

## AMENDMENTS

### In the Specification:

Please add the following paragraph on page 1 before the "Field of the Invention" section:

A 1  
The Sequence Listing (containing SEQ ID NOS:1-1613) is submitted in accordance with 37 CFR §§ 1.821-1.825 and §§1.52(e) and 1.96(c) on three compact discs labeled "Computer Readable Form (CRF)", "Copy 1" and "Copy 2", the contents of which are the same and are expressly incorporated herein by reference. The file names are A71249.ST25, contain 16,870,127 bytes, and were recorded on May 29, 2002.

Please replace the paragraph on page 9, starting at line 11 with the following:

(NE)  
A 2  
The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (SEQ ID NO:361) (W=tryptophan, S=serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Please replace the paragraph on page 11 starting at line 21 with the following:

(NE)  
A 3  
The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid (SEQ ID NO:1613) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Please amend the specification by replacing pages 52-196 with the following:

→ A4 ←



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example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the CA protein. When desired, tissue-specific expression or knockout of the CA protein may be necessary.

It is also possible that the CA protein is overexpressed in carcinoma. As such, transgenic animals can be generated that overexpress the CA protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of CA and are additionally useful in screening for bioactive molecules to treat carcinoma.

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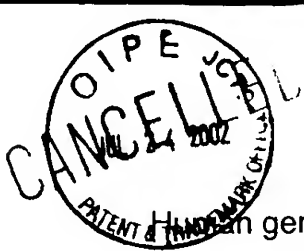
The CA nucleic acid sequences of the invention are depicted in Tables 1-112. The sequences in Tables 1 (SEQ ID NOS:1-460) and 2 (SEQ ID NOS:461-952) depict mouse tags, i.e. the genomic insertion sites. The sequences in Tables 3-112 (SEQ ID NOS:953-1612) include genomic sequence, mRNA and coding sequences for both mouse and human. N/A indicates a gene that has been identified, but for which there has not been a name ascribed. The different sequences of Tables 3-112 are assigned the following SEQ ID Nos:

Table 3 (mouse gene: Fscn1; human gene SNL)

- Mouse genomic sequence (SEQ ID NO:953)
- Mouse mRNA sequence (SEQ ID NO:954)
- Mouse coding sequence (SEQ ID NO:955)
- Human genomic sequence (SEQ ID NO:956)
- Human mRNA sequence (SEQ ID NO:957)
- Human coding sequence (SEQ ID NO:958)

Table 4 (mouse gene Map3k6; human gene MAP3K6)

- Mouse genomic sequence (SEQ ID NO:959)
- Mouse mRNA sequence (SEQ ID NO:960)
- Mouse coding sequence (SEQ ID NO:961)



Human genomic sequence (SEQ ID NO:962)

Human mRNA sequence (SEQ ID NO:963)

Human coding sequence (SEQ ID NO:964)

Table 5 (mouse gene Fosb; human gene FOSB)

Mouse genomic sequence (SEQ ID NO:965)

Mouse mRNA sequence (SEQ ID NO:966)

Mouse coding sequence (SEQ ID NO:967)

Human genomic sequence (SEQ ID NO:968)

Human mRNA sequence (SEQ ID NO:969)

Human coding sequence (SEQ ID NO:970)

Table 6 (mouse gene cmkbr7; human gene: CCR7)

Mouse genomic sequence (SEQ ID NO:971)

Mouse mRNA sequence (SEQ ID NO:972)

Mouse coding sequence (SEQ ID NO:973)

Human genomic sequence (SEQ ID NO:974)

Human mRNA sequence (SEQ ID NO:975)

Human coding sequence (SEQ ID NO:976)

Table 7 (mouse gene: Ccnd1; human gene: CCND1)

Mouse genomic sequence (SEQ ID NO:977)

Mouse mRNA sequence (SEQ ID NO:978)

Mouse coding sequence (SEQ ID NO:979)

Human genomic sequence (SEQ ID NO:980)

Human mRNA sequence (SEQ ID NO:981)

Human coding sequence (SEQ ID NO:982)

Table 8 (mouse gene: Ccnd3; human gene: CCND3)

Mouse genomic sequence (SEQ ID NO:983)

Mouse mRNA sequence (SEQ ID NO:984)

Mouse coding sequence (SEQ ID NO:985)  
Human genomic sequence (SEQ ID NO:986)  
Human mRNA sequence (SEQ ID NO:987)  
Human coding sequence (SEQ ID NO:988)

Table 9 (mouse gene: Wnt3; human gene: WNT3)

Mouse genomic sequence (SEQ ID NO:989)  
Mouse mRNA sequence (SEQ ID NO:990)  
Mouse coding sequence (SEQ ID NO:991)  
Human genomic sequence (SEQ ID NO:992)  
Human mRNA sequence (SEQ ID NO:993)  
Human coding sequence (SEQ ID NO:994)

Table 10 (mouse gene: Batf; human gene: BATF)

Mouse genomic sequence (SEQ ID NO:995)  
Mouse mRNA sequence (SEQ ID NO:996)  
Mouse coding sequence (SEQ ID NO:997)  
Human genomic sequence (SEQ ID NO:998)  
Human mRNA sequence (SEQ ID NO:999)  
Human coding sequence (SEQ ID NO:1000)

Table 11 (mouse gene: Irf4; human gene: IRF4)

Mouse genomic sequence (SEQ ID NO:1001)  
Mouse mRNA sequence (SEQ ID NO:1002)  
Mouse coding sequence (SEQ ID NO:1003)  
Human genomic sequence (SEQ ID NO:1004)  
Human mRNA sequence (SEQ ID NO:1005)  
Human coding sequence (SEQ ID NO:1006)

Table 12 (mouse gene: Notch1; human gene: NOTCH1)

Mouse genomic sequence (SEQ ID NO:1007)



Mouse mRNA sequence (SEQ ID NO:1008)  
Mouse coding sequence (SEQ ID NO:1009)  
Human genomic sequence (SEQ ID NO:1010)  
Human mRNA sequence (SEQ ID NO:1011)  
Human coding sequence (SEQ ID NO:1012)

Table 13 (mouse gene: Myc; human gene MYC)

Mouse genomic sequence (SEQ ID NO:1013)  
Mouse mRNA sequence (SEQ ID NO:1014)  
Mouse coding sequence (SEQ ID NO:1015)  
Human genomic sequence (SEQ ID NO:1016)  
Human mRNA sequence (SEQ ID NO:1017)  
Human coding sequence (SEQ ID NO:1018)

Table 14 (mouse gene Bach2; human gene BACH2)

Mouse genomic sequence (SEQ ID NO:1019)  
Mouse mRNA sequence (SEQ ID NO:1020)  
Mouse coding sequence (SEQ ID NO:1021)  
Human genomic sequence (SEQ ID NO:1022)  
Human mRNA sequence (SEQ ID NO:1023)  
Human coding sequence (SEQ ID NO:1024)

Table 15 (mouse gene Wnt1; human gene WNT1)

Mouse genomic sequence (SEQ ID NO:1025)  
Mouse mRNA sequence (SEQ ID NO:1026)  
Mouse coding sequence (SEQ ID NO:1027)  
Human genomic sequence (SEQ ID NO:1028)  
Human mRNA sequence (SEQ ID NO:1029)  
Human coding sequence (SEQ ID NO:1030)

Table 16 (mouse gene Rasgrp1; human gene: RASGRP1)

Mouse genomic sequence (SEQ ID NO:1031)

Mouse mRNA sequence (SEQ ID NO:1032)

Mouse coding sequence (SEQ ID NO:1033)

Human genomic sequence (SEQ ID NO:1034)

Human mRNA sequence (SEQ ID NO:1035)

Human coding sequence (SEQ ID NO:1036)

Table 17 (mouse gene: Nmyc1; human gene: MYCN)

Mouse genomic sequence (SEQ ID NO:1037)

Mouse mRNA sequence (SEQ ID NO:1038)

Mouse coding sequence (SEQ ID NO:1039)

Human genomic sequence (SEQ ID NO:1040)

Human mRNA sequence (SEQ ID NO:1041)

Human coding sequence (SEQ ID NO:1042)

Table 18 (mouse gene: Myb; human gene: MYB)

Mouse genomic sequence (SEQ ID NO:1043)

Mouse mRNA sequence (SEQ ID NO:1044)

Mouse coding sequence (SEQ ID NO:1045)

Human genomic sequence (SEQ ID NO:1046)

Human mRNA sequence (SEQ ID NO:1047)

Human coding sequence (SEQ ID NO:1048)

Table 19 (mouse gene: Sox4; human gene: SOX4)

Mouse genomic sequence (SEQ ID NO:1049)

Mouse mRNA sequence (SEQ ID NO:1050)

Mouse coding sequence (SEQ ID NO:1051)

Human genomic sequence (SEQ ID NO:1052)

Human mRNA sequence (SEQ ID NO:1053)

Human coding sequence (SEQ ID NO:1054)

Table 20 (mouse gene: Tcof1; human gene: TCOF1)

Mouse genomic sequence (SEQ ID NO:1055)

Mouse mRNA sequence (SEQ ID NO:1056)

Mouse coding sequence (SEQ ID NO:1057)

Human genomic sequence (SEQ ID NO:1058)

Human mRNA sequence (SEQ ID NO:1059)

Human coding sequence (SEQ ID NO:1060)

Table 21 (mouse gene: Pim1; human gene: PIM1)

Mouse genomic sequence (SEQ ID NO:1061)

Mouse mRNA sequence (SEQ ID NO:1062)

Mouse coding sequence (SEQ ID NO:1063)

Human genomic sequence (SEQ ID NO:1064)

Human mRNA sequence (SEQ ID NO:1065)

Human coding sequence (SEQ ID NO:1066)

Table 22 (mouse gene: Wnt3a; human gene: WNT3A)

Mouse genomic sequence (SEQ ID NO:1067)

Mouse mRNA sequence (SEQ ID NO:1068)

Mouse coding sequence (SEQ ID NO:1069)

Human genomic sequence (SEQ ID NO:1070)

Human mRNA sequence (SEQ ID NO:1071)

Human coding sequence (SEQ ID NO:1072)

Table 23 (mouse gene: Ly6e; human gene LY6E)

Mouse genomic sequence (SEQ ID NO:1073)

Mouse mRNA sequence (SEQ ID NO:1074)

Mouse coding sequence (SEQ ID NO:1075)

Human genomic sequence (SEQ ID NO:1076)

Human mRNA sequence (SEQ ID NO:1077)

Human coding sequence (SEQ ID NO:1078)

Table 24 (mouse gene: Rasa2; human gene RASA2)

Mouse genomic sequence (SEQ ID NO:1079)

Mouse mRNA sequence (SEQ ID NO:1080)

Mouse coding sequence (SEQ ID NO:1081)

Human genomic sequence (SEQ ID NO:1082)

Human mRNA sequence (SEQ ID NO:1083)

Human coding sequence (SEQ ID NO:1084)

Table 25 (mouse gene: Gata1; human gene GATA1)

Mouse genomic sequence (SEQ ID NO:1085)

Mouse mRNA sequence (SEQ ID NO:1086)

Mouse coding sequence (SEQ ID NO:1087)

Human genomic sequence (SEQ ID NO:1088)

Human mRNA sequence (SEQ ID NO:1089)

Human coding sequence (SEQ ID NO:1090)

Table 26 (mouse gene: Fkbp5; human gene FKBP5)

Mouse genomic sequence (SEQ ID NO:1091)

Mouse mRNA sequence (SEQ ID NO:1092)

Mouse coding sequence (SEQ ID NO:1093)

Human genomic sequence (SEQ ID NO:1094)

Human mRNA sequence (SEQ ID NO:1095)

Human coding sequence (SEQ ID NO:1096)

Table 27 (mouse gene: Rel; human gene REL)

Mouse genomic sequence (SEQ ID NO:1097)

Mouse mRNA sequence (SEQ ID NO:1098)

Mouse coding sequence (SEQ ID NO:1099)

Human genomic sequence (SEQ ID NO:1100)

Human mRNA sequence (SEQ ID NO:1101)

Human coding sequence (SEQ ID NO:1102)

Table 28 (mouse gene: Icsbp; human gene ICSBP1)

Mouse genomic sequence (SEQ ID NO:1103)

Mouse mRNA sequence (SEQ ID NO:1104)

Mouse coding sequence (SEQ ID NO:1105)

Human genomic sequence (SEQ ID NO:1106)

Human mRNA sequence (SEQ ID NO:1107)

Human coding sequence (SEQ ID NO:1108)

Table 29 (mouse gene: Bmi1; human gene BMI1)

Mouse genomic sequence (SEQ ID NO:1109)

Mouse mRNA sequence (SEQ ID NO:1110)

Mouse coding sequence (SEQ ID NO:1111)

Human genomic sequence (SEQ ID NO:1112)

Human mRNA sequence (SEQ ID NO:1113)

Human coding sequence (SEQ ID NO:1114)

Table 30 (mouse gene: Runx1; human gene RUNX1)

Mouse genomic sequence (SEQ ID NO:1115)

Mouse mRNA sequence (SEQ ID NO:1116)

Mouse coding sequence (SEQ ID NO:1117)

Human genomic sequence (SEQ ID NO:1118)

Human mRNA sequence (SEQ ID NO:1119)

Human coding sequence (SEQ ID NO:1120)

Table 31 (mouse gene: Il2ra; human gene IL2RA)

Mouse genomic sequence (SEQ ID NO:1121)

Mouse mRNA sequence (SEQ ID NO:1122)

Mouse coding sequence (SEQ ID NO:1123)

Human genomic sequence (SEQ ID NO:1124)

Human mRNA sequence (SEQ ID NO:1125)

Human coding sequence (SEQ ID NO:1126)

Table 32 (mouse gene: Nfkb1; human gene NFKB1)

Mouse genomic sequence (SEQ ID NO:1127)

Mouse mRNA sequence (SEQ ID NO:1128)

Mouse coding sequence (SEQ ID NO:1129)

Human genomic sequence (SEQ ID NO:1130)

Human mRNA sequence (SEQ ID NO:1131)

Human coding sequence (SEQ ID NO:1132)

Table 33 (mouse gene: Fyn; human gene FYN)

Mouse genomic sequence (SEQ ID NO:1133)

Mouse mRNA sequence (SEQ ID NO:1134)

Mouse coding sequence (SEQ ID NO:1135)

Human genomic sequence (SEQ ID NO:1136)

Human mRNA sequence (SEQ ID NO:1137)

Human coding sequence (SEQ ID NO:1138)

Table 34 (mouse gene: Nfkbil1; human gene NFKBIL1)

Mouse genomic sequence (SEQ ID NO:1139)

Mouse mRNA sequence (SEQ ID NO:1140)

Mouse coding sequence (SEQ ID NO:1141)

Human genomic sequence (SEQ ID NO:1142)

Human mRNA sequence (SEQ ID NO:1143)

Human coding sequence (SEQ ID NO:1144)

Table 35 (mouse gene: Flt3; human gene FLT3)

Mouse genomic sequence (SEQ ID NO:1145)

Mouse mRNA sequence (SEQ ID NO:1146)

Mouse coding sequence (SEQ ID NO:1147)

Human genomic sequence (SEQ ID NO:1148)

Human mRNA sequence (SEQ ID NO:1149)

Human coding sequence (SEQ ID NO:1150)

Table 36 (mouse gene: Dnnt; human gene DNNT)

Mouse genomic sequence (SEQ ID NO:1151)

Mouse mRNA sequence (SEQ ID NO:1152)

Mouse coding sequence (SEQ ID NO:1153)

Human genomic sequence (SEQ ID NO:1154)

Human mRNA sequence (SEQ ID NO:1155)

Human coding sequence (SEQ ID NO:1156)

Table 37 (mouse gene: Znfn1a1; human gene ZNFN1A1)

Mouse genomic sequence (SEQ ID NO:1157)

Mouse mRNA sequence (SEQ ID NO:1158)

Mouse coding sequence (SEQ ID NO:1159)

Human genomic sequence (SEQ ID NO:1160)

Human mRNA sequence (SEQ ID NO:1161)

Human coding sequence (SEQ ID NO:1162)

Table 38 (mouse gene: Tbx21; human gene TBX21)

Mouse genomic sequence (SEQ ID NO:1163)

Mouse mRNA sequence (SEQ ID NO:1164)

Mouse coding sequence (SEQ ID NO:1165)

Human genomic sequence (SEQ ID NO:1166)

Human mRNA sequence (SEQ ID NO:1167)

Human coding sequence (SEQ ID NO:1168)

Table 39 (mouse gene: Stat5b; human gene STAT5B)

Mouse genomic sequence (SEQ ID NO:1169)

Mouse mRNA sequence (SEQ ID NO:1170)

Mouse coding sequence (SEQ ID NO:1171)  
Human genomic sequence (SEQ ID NO:1172)  
Human mRNA sequence (SEQ ID NO:1173)  
Human coding sequence (SEQ ID NO:1174)

Table 40 (mouse gene: Sema4d; human gene SEMA4D)

Mouse genomic sequence (SEQ ID NO:1175)  
Mouse mRNA sequence (SEQ ID NO:1176)  
Mouse coding sequence (SEQ ID NO 1177)  
Human genomic sequence (SEQ ID NO 1178)  
Human mRNA sequence (SEQ ID NO:1179)  
Human coding sequence (SEQ ID NO:1180)

Table 41 (mouse gene: Mdm2; human gene MDM2)

Mouse genomic sequence (SEQ ID NO:1181)  
Mouse mRNA sequence (SEQ ID NO:1182)  
Mouse coding sequence (SEQ ID NO:1183)  
Human genomic sequence (SEQ ID NO:1184)  
Human mRNA sequence (SEQ ID NO:1185)  
Human coding sequence (SEQ ID NO:1186)

Table 42 (mouse gene: Prlr; human gene PRLR)

Mouse genomic sequence (SEQ ID NO:1187)  
Mouse mRNA sequence (SEQ ID NO:1188)  
Mouse coding sequence (SEQ ID NO:1189)  
Human genomic sequence (SEQ ID NO:1190)  
Human mRNA sequence (SEQ ID NO:1191)  
Human coding sequence (SEQ ID NO:1192)

Table 43 (mouse gene: Top1; human gene TOP1)

Mouse genomic sequence (SEQ ID NO:1193)



Mouse mRNA sequence (SEQ ID NO:1194)  
Mouse coding sequence (SEQ ID NO:1195)  
Human genomic sequence (SEQ ID NO:1196)  
Human mRNA sequence (SEQ ID NO:1197)  
Human coding sequence (SEQ ID NO:1198)

Table 44 (mouse gene: Dusp10; human gene DUSP10)

Mouse genomic sequence (SEQ ID NO:1199)  
Mouse mRNA sequence (SEQ ID NO:1200)  
Mouse coding sequence (SEQ ID NO:1201)  
Human genomic sequence (SEQ ID NO:1202)  
Human mRNA sequence (SEQ ID NO:1203)  
Human coding sequence (SEQ ID NO:1204)

Table 45 (mouse gene: Fli1; human gene FLI1)

Mouse genomic sequence (SEQ ID NO:1205)  
Mouse mRNA sequence (SEQ ID NO:1206)  
Mouse coding sequence (SEQ ID NO:1207)  
Human genomic sequence (SEQ ID NO:1208)  
Human mRNA sequence (SEQ ID NO:1209)  
Human coding sequence (SEQ ID NO:1210)

Table 46 (mouse gene: Tk2; human gene TK2)

Mouse genomic sequence (SEQ ID NO:1211)  
Mouse mRNA sequence (SEQ ID NO:1212)  
Mouse coding sequence (SEQ ID NO:1213)  
Human genomic sequence (SEQ ID NO:1214)  
Human mRNA sequence (SEQ ID NO:1215)  
Human coding sequence (SEQ ID NO:1216)

Table 47 (mouse gene: Nupr1)

Mouse genomic sequence (SEQ ID NO:1217)

Mouse mRNA sequence (SEQ ID NO:1218)

Mouse coding sequence (SEQ ID NO:1219)

Human genomic sequence (SEQ ID NO:1220)

Human mRNA sequence (SEQ ID NO:1221)

Human coding sequence (SEQ ID NO:1222)

Table 48 (mouse gene: Zfhx1b; human gene ZFHX1B)

Mouse genomic sequence (SEQ ID NO:1223)

Mouse mRNA sequence (SEQ ID NO:1224)

Mouse coding sequence (SEQ ID NO:1225)

Human genomic sequence (SEQ ID NO:1226)

Human mRNA sequence (SEQ ID NO:1227)

Human coding sequence (SEQ ID NO:1228)

Table 49 (mouse gene: Vdac1; human gene VDAC1)

Mouse genomic sequence (SEQ ID NO:1229)

Mouse mRNA sequence (SEQ ID NO:1230)

Mouse coding sequence (SEQ ID NO:1231)

Human genomic sequence (SEQ ID NO:1232)

Human mRNA sequence (SEQ ID NO:1233)

Human coding sequence (SEQ ID NO:1234)

Table 50 (mouse gene: Nfatc1; human gene NFATC1)

Mouse genomic sequence (SEQ ID NO:1235)

Mouse mRNA sequence (SEQ ID NO:1236)

Mouse coding sequence (SEQ ID NO:1237)

Human genomic sequence (SEQ ID NO:1238)

Human mRNA sequence (SEQ ID NO:1239)

Human coding sequence (SEQ ID NO:1240)

Table 51 (mouse gene: Syk; human gene SYK)

Mouse genomic sequence (SEQ ID NO:1241)

Mouse mRNA sequence (SEQ ID NO:1242)

Mouse coding sequence (SEQ ID NO:1243)

Human genomic sequence (SEQ ID NO:1244)

Human mRNA sequence (SEQ ID NO:1245)

Human coding sequence (SEQ ID NO:1246)

Table 52 (mouse gene: Gnb1; human gene GNB1)

Mouse genomic sequence (SEQ ID NO:1247)

Mouse mRNA sequence (SEQ ID NO:1248)

Mouse coding sequence (SEQ ID NO:1249)

Human genomic sequence (SEQ ID NO:1250)

Human mRNA sequence (SEQ ID NO:1251)

Human coding sequence (SEQ ID NO:1252).

Table 53 (mouse gene: Ccnd2; human gene CCND2)

Mouse genomic sequence (SEQ ID NO:1253)

Mouse mRNA sequence (SEQ ID NO:1254)

Mouse coding sequence (SEQ ID NO:1255)

Human genomic sequence (SEQ ID NO:1256)

Human mRNA sequence (SEQ ID NO:1257)

Human coding sequence (SEQ ID NO:1258)

Table 54 (mouse gene Tnfrsf6; human gene TNFRSF6)

Mouse genomic sequence (SEQ ID NO:1259)

Mouse mRNA sequence (SEQ ID NO:1260)

Mouse coding sequence (SEQ ID NO:1261)

Human genomic sequence (SEQ ID NO:1262)

Human mRNA sequence (SEQ ID NO:1263)

Human coding sequence (SEQ ID NO:1264)

Table 55 (mouse gene Irf2; human gene IRF2)

Mouse genomic sequence (SEQ ID NO:1265)

Mouse mRNA sequence (SEQ ID NO:1266)

Mouse coding sequence (SEQ ID NO:1267)

Human genomic sequence (SEQ ID NO:1268)

Human mRNA sequence (SEQ ID NO:1269)

Human coding sequence (SEQ ID NO:1270)

Table 56 (mouse gene Morf; human gene: MORF)

Mouse genomic sequence (SEQ ID NO:1271)

Mouse mRNA sequence (SEQ ID NO:1272)

Mouse coding sequence (SEQ ID NO:1273)

Human genomic sequence (SEQ ID NO:1274)

Human mRNA sequence (SEQ ID NO:1275)

Human coding sequence (SEQ ID NO:1276)

Table 57 (mouse gene: Runx3; human gene: RUNX3)

Mouse genomic sequence (SEQ ID NO:1277)

Mouse mRNA sequence (SEQ ID NO:1278)

Mouse coding sequence (SEQ ID NO:1279)

Human genomic sequence (SEQ ID NO:1280)

Human mRNA sequence (SEQ ID NO:1281)

Human coding sequence (SEQ ID NO:1282)

Table 58 (mouse gene: Bcl11b; human gene: BCL11B)

Mouse genomic sequence (SEQ ID NO:1283)

Mouse mRNA sequence (SEQ ID NO:1284)

Mouse coding sequence (SEQ ID NO:1285)

Human genomic sequence (SEQ ID NO:1286)

Human mRNA sequence (SEQ ID NO:1287)

Human coding sequence (SEQ ID NO:1288)

Table 59 (mouse gene: Arhgef1; human gene: ARHGEF1)

Mouse genomic sequence (SEQ ID NO:1289)

Mouse mRNA sequence (SEQ ID NO:1290)

Mouse coding sequence (SEQ ID NO:1291)

Human genomic sequence (SEQ ID NO:1292)

Human mRNA sequence (SEQ ID NO:1293)

Human coding sequence (SEQ ID NO:1294)

Table 60 (mouse gene: Ptpk; human gene: PTPRK)

Mouse genomic sequence (SEQ ID NO:1295)

Mouse mRNA sequence (SEQ ID NO:1296)

Mouse coding sequence (SEQ ID NO:1297)

Human genomic sequence (SEQ ID NO:1298)

Human mRNA sequence (SEQ ID NO:1299)

Human coding sequence (SEQ ID NO:1300)

Table 61 (mouse gene: Mcmd5; human gene: MCM5)

Mouse genomic sequence (SEQ ID NO:1301)

Mouse mRNA sequence (SEQ ID NO:1302)

Mouse coding sequence (SEQ ID NO:1303)

Human genomic sequence (SEQ ID NO:1304)

Human mRNA sequence (SEQ ID NO:1305)

Human coding sequence (SEQ ID NO:1306)

Table 62 (mouse gene: Matn4; human gene: MATN4)

Mouse genomic sequence (SEQ ID NO:1307)

Mouse mRNA sequence (SEQ ID NO:1308)

Mouse coding sequence (SEQ ID NO:1309)

Human genomic sequence (SEQ ID NO:1310)

Human mRNA sequence (SEQ ID NO:1311)

Human coding sequence (SEQ ID NO:1312)

Table 63 (mouse gene: Tnfsf11; human gene TNFSF11)

Mouse genomic sequence (SEQ ID NO:1313)

Mouse mRNA sequence (SEQ ID NO:1314)

Mouse coding sequence (SEQ ID NO:1315)

Human genomic sequence (SEQ ID NO:1316)

Human mRNA sequence (SEQ ID NO:1317)

Human coding sequence (SEQ ID NO:1318)

Table 64 (mouse gene: Itk; human gene ITK)

Mouse genomic sequence (SEQ ID NO:1319)

Mouse mRNA sequence (SEQ ID NO:1320)

Mouse coding sequence (SEQ ID NO:1321)

Human genomic sequence (SEQ ID NO:1322)

Human mRNA sequence (SEQ ID NO:1323)

Human coding sequence (SEQ ID NO:1324)

Table 65 (mouse gene: Fish; human gene: N/A)

Mouse genomic sequence (SEQ ID NO:1325)

Mouse mRNA sequence (SEQ ID NO:1326)

Mouse coding sequence (SEQ ID NO:1327)

Human genomic sequence (SEQ ID NO:1328)

Human mRNA sequence (SEQ ID NO:1329)

Human coding sequence (SEQ ID NO:1330)

Table 66 (mouse gene: Egr2; human gene EGR2)

Mouse genomic sequence (SEQ ID NO:1331)

Mouse mRNA sequence (SEQ ID NO:1332)

Mouse coding sequence (SEQ ID NO:1333)

Human genomic sequence (SEQ ID NO:1334)

Human mRNA sequence (SEQ ID NO:1335)

Human coding sequence (SEQ ID NO:1336)

Table 67 (mouse gene: Sos1; human gene SOS1)

Mouse genomic sequence (SEQ ID NO:1337)

Mouse mRNA sequence (SEQ ID NO:1338)

Mouse coding sequence (SEQ ID NO:1339)

Human genomic sequence (SEQ ID NO:1340)

Human mRNA sequence (SEQ ID NO:1341)

Human coding sequence (SEQ ID NO:1342)

Table 68 (mouse gene: Pou2af1; human gene POU2AF1)

Mouse genomic sequence (SEQ ID NO:1343)

Mouse mRNA sequence (SEQ ID NO:1344)

Mouse coding sequence (SEQ ID NO:1345)

Human genomic sequence (SEQ ID NO:1346)

Human mRNA sequence (SEQ ID NO:1347)

Human coding sequence (SEQ ID NO:1348)

Table 69 (mouse gene: Mef2c; human gene MEF2C)

Mouse genomic sequence (SEQ ID NO:1349)

Mouse mRNA sequence (SEQ ID NO:1350)

Mouse coding sequence (SEQ ID NO:1351)

Human genomic sequence (SEQ ID NO:1352)

Human mRNA sequence (SEQ ID NO:1353)

Human coding sequence (SEQ ID NO:1354)

Table 70 (mouse gene: Map3k8; human gene MAP3K8)

Mouse genomic sequence (SEQ ID NO:1355)

Mouse mRNA sequence (SEQ ID NO:1356)

Mouse coding sequence (SEQ ID NO:1357)  
Human genomic sequence (SEQ ID NO:1358)  
Human mRNA sequence (SEQ ID NO:1359)  
Human coding sequence (SEQ ID NO:1360)

Table 71 (mouse gene: Fgfr3; human gene FGFR3)

Mouse genomic sequence (SEQ ID NO:1361)  
Mouse mRNA sequence (SEQ ID NO:1362)  
Mouse coding sequence (SEQ ID NO:1363)  
Human genomic sequence (SEQ ID NO:1364)  
Human mRNA sequence (SEQ ID NO:1365)  
Human coding sequence (SEQ ID NO:1366)

Table 72 (mouse gene: Cbx8; human gene CBX8)

Mouse genomic sequence (SEQ ID NO:1367)  
Mouse mRNA sequence (SEQ ID NO:1368)  
Mouse coding sequence (SEQ ID NO:1369)  
Human genomic sequence (SEQ ID NO:1370)  
Human mRNA sequence (SEQ ID NO:1371)  
Human coding sequence (SEQ ID NO:1372)

Table 73 (mouse gene: Lmo2; human gene LMO2)

Mouse genomic sequence (SEQ ID NO:1373)  
Mouse mRNA sequence (SEQ ID NO:1374)  
Mouse coding sequence (SEQ ID NO:1375)  
Human genomic sequence (SEQ ID NO:1376)  
Human mRNA sequence (SEQ ID NO:1377)  
Human coding sequence (SEQ ID NO:1378)

Table 74 (mouse gene: Itpr1; human gene ITPR1)

Mouse genomic sequence (SEQ ID NO:1379)



Mouse mRNA sequence (SEQ ID NO:1380)  
Mouse coding sequence (SEQ ID NO:1381)  
Human genomic sequence (SEQ ID NO:1382)  
Human mRNA sequence (SEQ ID NO:1383)  
Human coding sequence (SEQ ID NO: 1384)

Table 75 (mouse gene: Sell; human gene SELL)

Mouse genomic sequence (SEQ ID NO:1385)  
Mouse mRNA sequence (SEQ ID NO:1386)  
Mouse coding sequence (SEQ ID NO:1387)  
Human genomic sequence (SEQ ID NO:1388)  
Human mRNA sequence (SEQ ID NO:1389)  
Human coding sequence (SEQ ID NO:1390)

Table 76 (mouse gene: Dpt; human gene DPT)

Mouse genomic sequence (SEQ ID NO:1391)  
Mouse mRNA sequence (SEQ ID NO:1392)  
Mouse coding sequence (SEQ ID NO:1393)  
Human genomic sequence (SEQ ID NO:1394)  
Human mRNA sequence (SEQ ID NO:1395)  
Human coding sequence (SEQ ID NO:1396)

Table 77 (mouse gene: Pap; human gene PAP)

Mouse genomic sequence (SEQ ID NO:1397)  
Mouse mRNA sequence (SEQ ID NO:1398)  
Mouse coding sequence (SEQ ID NO:1399)  
Human genomic sequence (SEQ ID NO:1400)  
Human mRNA sequence (SEQ ID NO:1401)  
Human coding sequence (SEQ ID NO:1402)

Table 78 (mouse gene: Blm; human gene BLM)

Mouse genomic sequence (SEQ ID NO:1403)  
Mouse mRNA sequence (SEQ ID NO:1404)  
Mouse coding sequence (SEQ ID NO:1405)  
Human genomic sequence (SEQ ID NO:1406)  
Human mRNA sequence (SEQ ID NO:1407)  
Human coding sequence (SEQ ID NO:1408)

Table 79 (mouse gene: Blr1; human gene BLR1)

Mouse genomic sequence (SEQ ID NO:1409)  
Mouse mRNA sequence (SEQ ID NO:1410)  
Mouse coding sequence (SEQ ID NO:1411)  
Human genomic sequence (SEQ ID NO:1412)  
Human mRNA sequence (SEQ ID NO:1413)  
Human coding sequence (SEQ ID NO:1414)

Table 80 (mouse gene: Ptp4a2; human gene PTP4A2)

Mouse genomic sequence (SEQ ID NO:1415)  
Mouse mRNA sequence (SEQ ID NO:1416)  
Mouse coding sequence (SEQ ID NO:1417)  
Human genomic sequence (SEQ ID NO:1418)  
Human mRNA sequence (SEQ ID NO:1419)  
Human coding sequence (SEQ ID NO:1420)

Table 81 (mouse gene: Mcm3ap; human gene MCM3AP)

Mouse genomic sequence (SEQ ID NO:1421)  
Mouse mRNA sequence (SEQ ID NO:1422)  
Mouse coding sequence (SEQ ID NO:1423)  
Human genomic sequence (SEQ ID NO:1424)  
Human mRNA sequence (SEQ ID NO:1425)  
Human coding sequence (SEQ ID NO:1426)

Table 82 (mouse gene: Jak2; human gene JAK2)

Mouse genomic sequence (SEQ ID NO:1427)

Mouse mRNA sequence (SEQ ID NO:1428)

Mouse coding sequence (SEQ ID NO:1429)

Human genomic sequence (SEQ ID NO:1430)

Human mRNA sequence (SEQ ID NO:1431)

Human coding sequence (SEQ ID NO:1432)

Table 83 (mouse gene: Fus1; human gene FUS1)

Mouse genomic sequence (SEQ ID NO:1433)

Mouse mRNA sequence (SEQ ID NO:1434)

Mouse coding sequence (SEQ ID NO:1435)

Human genomic sequence (SEQ ID NO:1436)

Human mRNA sequence (SEQ ID NO:1437)

Human coding sequence (SEQ ID NO:1438)

Table 84 (mouse gene: Rassf1; human gene RASSF1)

Mouse genomic sequence (SEQ ID NO:1439)

Mouse mRNA sequence (SEQ ID NO:1440)

Mouse coding sequence (SEQ ID NO:1441)

Human genomic sequence (SEQ ID NO:1442)

Human mRNA sequence (SEQ ID NO:1443)

Human coding sequence (SEQ ID NO:1444)

Table 85 (mouse gene: Pik3r1; human gene PIK3R1)

Mouse genomic sequence (SEQ ID NO:1445)

Mouse mRNA sequence (SEQ ID NO:1446)

Mouse coding sequence (SEQ ID NO:1447)

Human genomic sequence (SEQ ID NO:1448)

Human mRNA sequence (SEQ ID NO:1449)

Human coding sequence (SEQ ID NO:1450)

Table 86 (mouse gene: Braf; human gene BRAF)

Mouse genomic sequence (SEQ ID NO:1451)

Mouse mRNA sequence (SEQ ID NO:1452)

Mouse coding sequence (SEQ ID NO:1453)

Human genomic sequence (SEQ ID NO:1454)

Human mRNA sequence (SEQ ID NO:1455)

Human coding sequence (SEQ ID NO:1456)

Table 87 (mouse gene: Tle3; human gene: TLE3)

Mouse genomic sequence (SEQ ID NO:1457)

Mouse mRNA sequence (SEQ ID NO:1458)

Mouse coding sequence (SEQ ID NO:1459)

Human genomic sequence (SEQ ID NO:1460)

Human mRNA sequence (SEQ ID NO:1461)

Human coding sequence (SEQ ID NO:1462)

Table 88 (mouse gene: Nek2; human gene NEK2)

Mouse genomic sequence (SEQ ID NO:1463)

Mouse mRNA sequence (SEQ ID NO:1464)

Mouse coding sequence (SEQ ID NO:1465)

Human genomic sequence (SEQ ID NO:1466)

Human mRNA sequence (SEQ ID NO:1467)

Human coding sequence (SEQ ID NO:1468)

Table 89 (mouse gene: Nr3c1; human gene NR3C1)

Mouse genomic sequence (SEQ ID NO: 1469)

Mouse mRNA sequence (SEQ ID NO:1470)

Mouse coding sequence (SEQ ID NO:1471)

Human genomic sequence (SEQ ID NO:1472)

Human mRNA sequence (SEQ ID NO: 1473)

Human coding sequence (SEQ ID NO:1474)

Table 90 (mouse gene: Dad1; human gene DAD1)

Mouse genomic sequence (SEQ ID NO:1475)

Mouse mRNA sequence (SEQ ID NO:1476)

Mouse coding sequence (SEQ ID NO:1477)

Human genomic sequence (SEQ ID NO:1478)

Human mRNA sequence (SEQ ID NO:1479)

Human coding sequence (SEQ ID NO:1480)

Table 91 (mouse gene: Lck; human gene LCK)

Mouse genomic sequence (SEQ ID NO:1481)

Mouse mRNA sequence (SEQ ID NO:1482)

Mouse coding sequence (SEQ ID NO:1483)

Human genomic sequence (SEQ ID NO:1484)

Human mRNA sequence (SEQ ID NO:1485)

Human coding sequence (SEQ ID NO:1486)

Table 92 (mouse gene: Git2; human gene GIT2)

Mouse genomic sequence (SEQ ID NO:1487)

Mouse mRNA sequence (SEQ ID NO:1488)

Mouse coding sequence (SEQ ID NO:1489)

Human genomic sequence (SEQ ID NO:1490)

Human mRNA sequence (SEQ ID NO:1491)

Human coding sequence (SEQ ID NO:1492).

Table 93 (mouse gene: Anp32; human gene N/A)

Mouse genomic sequence (SEQ ID NO:1493)

Mouse mRNA sequence (SEQ ID NO:1494)

Mouse coding sequence (SEQ ID NO:1495)

Human genomic sequence (SEQ ID NO:1496)

Human mRNA sequence (SEQ ID NO:1497)  
Human coding sequence (SEQ ID NO:1498).

Table 94 (mouse gene: Map2k5; human gene MAP2K5)

Mouse genomic sequence (SEQ ID NO:1499)  
Mouse mRNA sequence (SEQ ID NO:1500)  
Mouse coding sequence (SEQ ID NO:1501)  
Human genomic sequence (SEQ ID NO:1502)  
Human mRNA sequence (SEQ ID NO:1503)  
Human coding sequence (SEQ ID NO:552 1504).

Table 95 (mouse gene: Cd28; human gene CD28)

Mouse genomic sequence (SEQ ID NO:1505)  
Mouse mRNA sequence (SEQ ID NO:1506)  
Mouse coding sequence (SEQ ID NO:1507)  
Human genomic sequence (SEQ ID NO:1508)  
Human mRNA sequence (SEQ ID NO: 1509)  
Human coding sequence (SEQ ID NO:1510).

Table 96 (mouse gene: Sept9; human gene Msf)

Mouse genomic sequence (SEQ ID NO:1511)  
Mouse mRNA sequence (SEQ ID NO:1512)  
Mouse coding sequence (SEQ ID NO:1513)  
Human genomic sequence (SEQ ID NO:1514)  
Human mRNA sequence (SEQ ID NO:1515)  
Human coding sequence (SEQ ID NO:1516).

Table 97 (mouse gene: Fzd10; human gene FZD10)

Mouse genomic sequence (SEQ ID NO:1517)  
Mouse mRNA sequence (SEQ ID NO:1518)  
Mouse coding sequence (SEQ ID NO:1519)

Human genomic sequence (SEQ ID NO:1520)

Human mRNA sequence (SEQ ID NO:1521)

Human coding sequence (SEQ ID NO:1522).

Table 98 (mouse gene: Calm2; human gene CALM2)

Mouse genomic sequence (SEQ ID NO:1523)

Mouse mRNA sequence (SEQ ID NO:1524)

Mouse coding sequence (SEQ ID NO:1525)

Human genomic sequence (SEQ ID NO:1526)

Human mRNA sequence (SEQ ID NO:1527)

Human coding sequence (SEQ ID NO:1528).

Table 99 (mouse gene: Ncf4; human gene NCF4)

Mouse genomic sequence (SEQ ID NO:1529)

Mouse mRNA sequence (SEQ ID NO:1530)

Mouse coding sequence (SEQ ID NO:1531)

Human genomic sequence (SEQ ID NO:1532)

Human mRNA sequence (SEQ ID NO:1533)

Human coding sequence (SEQ ID NO:1534).

Table 100 (mouse gene: Rac2; human gene RAC2)

Mouse genomic sequence (SEQ ID NO:1535)

Mouse mRNA sequence (SEQ ID NO:1536)

Mouse coding sequence (SEQ ID NO:1537)

Human genomic sequence (SEQ ID NO:1538)

Human mRNA sequence (SEQ ID NO:1539)

Human coding sequence (SEQ ID NO:1540).

Table 101 (mouse gene: Mbnl; human gene MBNL)

Mouse genomic sequence (SEQ ID NO:1541)

Mouse mRNA sequence (SEQ ID NO:1542)

Mouse coding sequence (SEQ ID NO:1543)  
Human genomic sequence (SEQ ID NO:1544)  
Human mRNA sequence (SEQ ID NO:1545)  
Human coding sequence (SEQ ID NO:1546).

Table 102 (mouse gene: mCG10516; human gene N/A)

Mouse genomic sequence (SEQ ID NO:1547)  
Mouse mRNA sequence (SEQ ID NO:1548)  
Mouse coding sequence (SEQ ID NO:1549)  
Human genomic sequence (SEQ ID NO:1550)  
Human mRNA sequence (SEQ ID NO:1551)  
Human coding sequence (SEQ ID NO:1552)

Table 103 (mouse gene: Rorc; human gene RORC)

Mouse genomic sequence (SEQ ID NO:1553)  
Mouse mRNA sequence (SEQ ID NO:1554)  
Mouse coding sequence (SEQ ID NO:1555)  
Human genomic sequence (SEQ ID NO:1556)  
Human mRNA sequence (SEQ ID NO:1557)  
Human coding sequence (SEQ ID NO:1558)

Table 104 (mouse gene mCG15938; human gene BAT1)

Mouse genomic sequence (SEQ ID NO:1559)  
Mouse mRNA sequence (SEQ ID NO:1560)  
Mouse coding sequence (SEQ ID NO:1561)  
Human genomic sequence (SEQ ID NO:1562)  
Human mRNA sequence (SEQ ID NO:1563)  
Human coding sequence (SEQ ID NO:1564)

Table 105 (mouse gene: Iqgap1; human gene IQGAP1)

Mouse genomic sequence (SEQ ID NO:1565)



Mouse mRNA sequence (SEQ ID NO:1566)  
Mouse coding sequence (SEQ ID NO:1567)  
Human genomic sequence (SEQ ID NO:1568)  
Human mRNA sequence (SEQ ID NO:1569)  
Human coding sequence (SEQ ID NO:1570)

Table 106 (mouse gene Zpf29; human gene: hCG27579)

Mouse genomic sequence (SEQ ID NO:1571)  
Mouse mRNA sequence (SEQ ID NO:1572)  
Mouse coding sequence (SEQ ID NO:1573)  
Human genomic sequence (SEQ ID NO:1574)  
Human mRNA sequence (SEQ ID NO:1575)  
Human coding sequence (SEQ ID NO:1576)

Table 107 (mouse gene: Kcnj9; human gene: KCNJ9)

Mouse genomic sequence (SEQ ID NO:1577)  
Mouse mRNA sequence (SEQ ID NO:1578)  
Mouse coding sequence (SEQ ID NO:1579)  
Human genomic sequence (SEQ ID NO:1580)  
Human mRNA sequence (SEQ ID NO:1581)  
Human coding sequence (SEQ ID NO:1582)

Table 108 (mouse gene: Ppp3cc; human gene: PPP3CC)

Mouse genomic sequence (SEQ ID NO:1583)  
Mouse mRNA sequence (SEQ ID NO:1584)  
Mouse coding sequence (SEQ ID NO:1585)  
Human genomic sequence (SEQ ID NO:1586)  
Human mRNA sequence (SEQ ID NO:1587)  
Human coding sequence (SEQ ID NO:1588)

Table 109 (mouse gene: mCG9110; human gene: hCG27579)

Mouse genomic sequence (SEQ ID NO:1589)  
Mouse mRNA sequence (SEQ ID NO:1590)  
Mouse coding sequence (SEQ ID NO:1591)  
Human genomic sequence (SEQ ID NO:1592)  
Human mRNA sequence (SEQ ID NO:1593)  
Human coding sequence (SEQ ID NO:1594)

Table 110 (mouse gene: mCG2257; human gene: PRDM11)

Mouse genomic sequence (SEQ ID NO:1595)  
Mouse mRNA sequence (SEQ ID NO:1596)  
Mouse coding sequence (SEQ ID NO:1597)  
Human genomic sequence (SEQ ID NO:1598)  
Human mRNA sequence (SEQ ID NO:1599)  
Human coding sequence (SEQ ID NO:1600)

Table 111 (mouse gene: mCG17918; human gene: hCG23764)

Mouse genomic sequence (SEQ ID NO:1601)  
Mouse mRNA sequence (SEQ ID NO:1602)  
Mouse coding sequence (SEQ ID NO:1603)  
Human genomic sequence (SEQ ID NO:1604)  
Human mRNA sequence (SEQ ID NO:1605)  
Human coding sequence (SEQ ID NO:1606)

Table 112 (mouse gene: Lfng; human gene: LFNG)

Mouse genomic sequence (SEQ ID NO:1607)  
Mouse mRNA sequence (SEQ ID NO:1608)  
Mouse coding sequence (SEQ ID NO:1609)  
Human genomic sequence (SEQ ID NO:1610)  
Human mRNA sequence (SEQ ID NO:1611)  
Human coding sequence (SEQ ID NO:1612).

Table 1

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
1	IM000619	GATCAAAGCAATCTCTATGTCTTTCTCTG CTGTCCTCCTCAGACATCTCCAGAGAGC TGGGATATTTTTCTTTCCCATTTGAGATT ATGAAGTTGTTTCTAGAGTGACATGACGC AGGTTGAAGGATAAGTACACAGGTCCCA AGGAACCAAGCGTTTTCACTGACGGTGA TGAGTCTTGTTCTGTGAGATTGTTGTGATT CTCAGCCTTTCTCTTCCCCTGTGTGTGCT CTTCATTTTCTGGTTCTGTCTGCCTAGCA CCTCCTGGGGAAGCTGCTGTGCTTT	p000632	A	<i>Spr</i>
2	IM000620	GATCTTTGGAGCCCAGTTGTTAATCATAA GAGCTGATATTTTGAAGAGTGTGTCAA CCTAGATGCACAGGGAAGCCAAAGCATT CAGCC	p000633	D	--
3	IM000621	ATATGACCACAAGGAAATAAGATAAAGT GTTCACTACTGAATTTATAATGAAAAGTGA TC	p000634	C	--
4	IM000622	GAACAGGCATGGCTTTACTTGTAACAATG AGGAAACCAAGGCAGAGATTGCAAAGCG GGTCCTACACGTTTGCTCCATGCCCTGC TTCTCTGACCACAGTGTACTGAGAATATG CTGAGCCCTAGTTCCTGGGGAGGAGGC AGAAGAGAGCAGCATCCTGCCCACTTGA AGGCGTGCACACATAGTTCCTGTCTGAT C	p000638	D	--
5	IM000623	GATCAGGAGACCACACCCAGCTAGCCTT CTCTGACTGGGTATCCTTGGTCAGCCAG CCTTTCTTCACCTCATGTTCTCATTTGCA AACTCACATGAACACTATTTGACCTACAC ACTTCATAAAGCTGTTTTTAGAAAGACGA GATAATACAGGAGGAACGCTACAATATT AAATGATATGTATTTATAT	p000639	D	--
6	IM000624	AGTGTTTAGGTCAGCTGGTGCAGGAGAA GCTTCTTGAGGAAGACGACCATCTGGCA AGGCCTGATGGTAGAAAATAATGGACTT CTCTCCAAGTGTAGGAAGTGTATGAT C	p000640	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
7	IM000625	ATCAGTAAGTTAATCCTAAGAATTACTAT GCATTTTTCCCCTCTTTTTTAACAACATT CTCCTTAGCTTATATGAGGCTCTAGTGC CCGGAGACTTTAATACTGCCCTAACATG ATGGTGGCTCTTTGTCCCTCTTCTCAGC CACTGAAATCTGACAGTTTGGGGAAGAA TAATAAGAATTTAAGAACTAGATGGTTT TAAATATAGATATAAAAAACAGTTCTTCGA CTATTCTCAATAAAGAAATTCAGTCAAAA GAATTCAGTCCTAACACAATGATC	p000641	D	--
8	IM000626	GATCATCAGAGTCCTGCATCTTATGTGT GCAGTGTTTTCAGCAATACAGGCTTACC TTCAACCTCTAACAGGCAACCAGATGCT ACAATAGCTTATATTGTTTTAGAAATCAC TTGGACTACTCTAAACAACAACCTTGAGTG AAGGCTCTTTGTATCTGATACTGGAGTTT GTTAGTCTATGACACTTGTGGGGAGACA TGTCTGCACAAGTAGCATATGTGTGTAC ATGTATATTGTATACATATATAGTTTGCT CTATGTATGTATGTGTATATGTATGTATG TATATGTATATGTATGTATATATATAG	p000642	D	--
9	IM000627	AAGGGACCTGATAATCGTGTTGGCAACT GGGCTACAATTAGTTATCAATTGCTTGCT TGCCACCTGCCCTGCTCCATAGAGAATC ATAGTCTGGGGAGTGTGGAGGAATAGC GGAGTCATCTAAACACATCACTGCTGCC CCCACCATTTGCCTGCCACCAGGCCCTT GCCTTTCATTTTGCATTTCTCCCTCTTAC AAGCAAATGGCGCTCACTGATC	p000643	D	--
10	IM000628	GTTTGGGGATTGTACAGAATGCACAGCG TAGTATTCAGGAAAAAGGAACTGGGAA ATTAATGTATAAATTAAATCAGCTTTTAA TTAGCTTAACACACACATACGAAGGCAA AAATGTAACGTTACTTTGATC	p000644	K	<i>Myc</i>
11	IM000629	GATCTCATTACAGATGGTTGTGAGCTAC CATGTGG	p000647	R	--
12	IM000630	GATCTCAGGAGGCACCGAGAGACTCAG CATGGACTCAAATGAGTACCCTGGCAGC CCGCAACACCAGCTGTGTAACACTACCG TGAGGGATGTCTTCCCTGCCTCCCTCCA GCCCCTTCTCAGGCCCTGAGTCCAGTGT GCAAAGCTCATCATGGTTAGTCCCCTTC ACCT	p000649	K	<i>Gfi1</i>

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
13	IM000631	AGAGCACCCGACTGCTCTTCCGAAGGTC CAGAGTTCAAATCCCAGCAACCACATGG TGGCTCACAACCATCCGTAACAAGATC	p000650	R	--
14	IM000632	GATCAAATCCTGTCAGGGAGAGGGGCTC CTCCCAGTAGTGCCATCCCATAATAATAA GAAGGACTCCTGGGCCTCAGTGAAGTCA GGCTGACCACTACTGCAGGTTAGTCATG ACCAGTAGCCAGAATGGAACGAAGGGT GACCCAGTGTGAGGACACAGCCCCAGG CAACTGCTTCTGCTTTGAGCCAAGTTGTT ACCCCAAAGCTCGTCATTCCGCTTGTT TCTCATGTGTGTGAGCTGCACATATGGA GGTCCCCCTTTGTTCCCTT	p000651	D	--
15	IM000633	GTGAGGAAGGTCCCTCTGCATTCTAACC TTCCTCAACTCCACCAGCCTCGGCGTTT AAGGGAGAAATATTACCGTTCCCTTTGG GCCAAGTTGGAGCCAGTGAAGTAGTCG GAAATGTACAGTCACAGGAAATTGCTGC TACCAAGGCTGGAGGAACAAAGAGAAGA CTTGTCAAGAGAGGCCAGAGAGGAAGTC ACCCAGTACAACTGAAGCGCGCGCGC ACACACACACACACACACACACACGC ACACACACACACACACGATC	p000652	D	--
16	IM000634	TGGCCGCCTAGACAAGCTGACCATCACC TCCCAGAACCTGCAACTGGAGAGCCTTC GCATGAAGCTTCCGAAATGTGCGTGCTC CACCTGTCCCTCACCTCACAGACATCAT TTCTCCATTTAGCCCCCTCCCGATC	p000654	A	<i>li</i>
17	IM000635	GATCCCCTGGAATTTACAGTCGGTTCCA ACAATCATGTAGATG	p000656	C	--
18	IM000636	GATCGGCTATAGCATTTGTCAATGTTTAC CCAGAAGAATAGCACAGATATATTTGCA CATCAATGCTTATTGCAGTATTATTCACA GTGGCTATGTAATGGAACCAACCTACAT GGCCAGCAACTGAATAGATTAAGAAAAT ATATATACACAATGGTGCTTTTTTCGGCT ATAAAGAAGAATGAAGTTATGTTGTTTGT TAGAAGATGGATGAAAGTGGAGATGATA ATATCAAGTGCACAGTCAACCTCTCTCTC TCACCTCCCCCGCCCCGCTCTTTCTCTC TCATATACATTTGAGAGTAGCAGTAACT GTCTGAGAACAAAGGGGATTAATGGGAG GGGAGAAGATTAAGGAGCGGAAGGGTA GTAGGTAGTAT	p000659	A	<i>Cr2</i>

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
19	IM000637	GATCGGCTTCTATGGACTGAGTGTGTAA GAAAACATT	p000661	D	--
20	IM000638	TTAGGAGGGTAGAGAACATTCAGGAATC AAGAACAAGCATTTTAACACCCACTGAG CTATCCTGTGGATGGTGGTGGTTTTGTTT GTTTGTGGTTTTGTTTTAGGAAGTCAGG GATGGGGTGGGAATCTCACTCTGTGGCT TAGACTTGCAACAATCCCAAATTCTGGAA TGATAAGCAAGAGAGCTGTCTAGTCCCA GTCTCAGATACATGCTGTTAATTTTCTAC TACTGCTATAACACATAGGCTCAAATGC GGTGGCTTACCTAACACACCCTGTGCAG TTCTGAAAGTCGTAACCTCTGGCACGATC	p000662	D	--
21	IM000639	ATGCTAAGCTGTGACTCCTCTCGATACG AGACCCTGGCTGCCCTCCTTTCCCGATC	p000663	D	--
22	IM000640	GATCGTCTGGAAGAGCAGTCAGTATTCT TAACTGCTGAGCCATCTTTGCAGCCCCC AGTTCTTTGGGGTTTTTTGTTTGTTGTTT GGTTGGTTGGTTGGTTGGTTAGTTTG GTTTGGTTCAAGACAGGGTTTCTCTGTG TTGCCCTGGATGTCCTGGAACCTCTCTT GTAGACCAGGGTGGCCTTTAACTCACAG AAATGCGCCTGCTAGGATTAAAGCTGTG TCCCACCACTATATATATATGTGTG	p000665	R	--
23	IM000641	GTCACAGTGTTAGAGCCACAGACGGGG GAACCTACTGGCTGTCCTGGGTTCCTGT AACTAGGGGACAAAGCTGCCACAGCCA GACTTAGCTGCGATC	p000666	D	--
24	IM000642	GATCGCTGCTTCTGTAAATCCGCAACGA CAATTGTTATCTTCTCTTTTCTTTCTTTT ATTTGTTTTATTCTATTTATTTTCAGAT GAACTCTCATGTAGCCCAGGCTGGTCTC AAACTCCCTCTGTAGCTGACGGCAACCT TGAAC	p000668	R	--
25	IM000643	TTCCTACACCATAGCATTTAGTTGTAGGC AGAAGCGATC	p000669	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
26	IM000644	GATCGGCTCAAGGGCTCTAATTTAGTCT AGGAAGTCCTTAGGAAACATGAAAATCT CCGAGATAAGACCCGGGTAAAAAGCTT GAGCCACGGAGTTAGACATGCCAGGG TGGAGTCATGTTCAAGAGGTTCAAGACCC GAATCAGCTACGTAAATAAAGCATTGAG GCCTACCTGGGCTACAAGAGAGTATCTT TAAATAAATAAGATGATTTAAAAAAACT GTTTTCCCCTTAGATGGATTAAAAAACA AGACAAAACAAAACAAAACAAAACCCG TCTTTCCTTCTTAA	p000672	D	--
27	IM000645	CTGTCCGTGTGGGAAACGTTTAGCAAGT CCGAGCGTGTTGATC	p000673	K	Nmyc
28	IM000646	ATGCGTTCGTATGACAGTTCTCCAAATGA CTGTCCCAAAGTCCCAGATTCCTGGAAA CAGTAAAGACTGCCTCAAACGTAGTCA CTAGTCTATTATCTTAATCATAGTAACCA TTTGGGTTTGACTTGAAAACCTGTGACA GGGAGATAAATTTCTGCCACTGTAGGTG AAGCTTGGAAGGGCTAACCCAATGAATA TGCTCAGTCGATC	p000676	C	--
29	IM000647	AGATGAAGCTATCCCCAGTCCCTAAGCT GAGTTCTGCCTGAGACTATTTGAAACAG GGTACCCCTGGGTCCCAGTTCAGTTGAC AGGTAGTGGACGCATGAGAACGCCATAC CTGGTGGCCGTGCCCGAGAGTGCTGTC CCTGACCTGCCACTGTGTTCTCCAGAGC AGCTTTCGAATCTGCCTGCTCCTGTCTC CCCTGCCTGTTGGCACCAGGCAGCCAG AATTCCATTTGTTTGTTTGCTTCGCGATA GGCTCTTGCCATGTAGTCCTTCCTGGCC TAGAACTTGATATGTAGACTTCCCCCCTT GGATC	p000678	C	--
30	IM000648	CCGTGTCCGTGGGCATGTGCGTGTACA GACAGACATACATGCCCCCGCATGAGTG TGAACACCAGAGGTCAACCTCAGGTGTC CTTTTGATGTTATCTACCTTGTTTTTGAA GCAAGGTCTAGGATTGACCAATGAGCCC CAAGTAGGGATC	p000679	D	--
31	IM000649	GATCCATAGGCAGAGAAGGCAGTAATAG GACATTGGTCATTGTACCTCATTTGTGAG GGGTCACCTTGGAATGTGCTGAGACTA GGTTCTAGGAGAAGCTCGCCA	p000682	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
32	IM000650	CTGGCACTGTGTGGCAGAAACAGTGAAC AGTGTAGCGGTGCAGAATGTGTGTGCTG TGGGTTTTAGCACCAGGGCTGCATGAGA CTGCAGACATGCTTATGACGCAGGAAGG CTCAGGACACAGCACACATGTGTGCTAA CATACATGTTTCACCTCAGACTCAGCTCC CATTTGACTTTTAATTAATTTTTGGCCATT CCACAACAGAACCTTTTCTTGCTCCCTTT TTTCAATCTTATGTATATATCTCCTACATT TAGTTACAGGACTGTGACCTACAGTTTAA AACTCGGGGATC	p000684	D	--
33	IM000651	GATCCCTCCCCTCCCTTCTTTTTCCCGC CAAGCGTCGGCGAAGCCCTGCCCTTCA GGAGGCAGGAGGGGAGCTGAGTGAGGC GAGTCGGACCCAGCAGCTGAGAGCAGC GCAGCCCAGGGGTCTCGGCCGCGCAG ACCCCCGGAATAA	p000685	K	<i>Myc</i>
34	IM000652	CTACCACAGCCCCAGTGCTCTGGAGGG ACTCTAGTAGCCAGGGCTGGCAGCTTGG TTTGGGCCAGCATCTCACTATGTAGCCT AGTTGTCCTGGAATTTGCTATGTAAATGT GGCTACCCTCAAACCATAGAGAGCCTC CCACCTCTCCTGAGATTATAGGCACATG CTACCATGCCCTAAGTGGATC	p000686	D	--
35	IM000653	GGAGCAGGCCCTTCTGAATCAACTTGGC AGAGTGAAGGAGGCACTCTCCACACAAA CAGGAAAAGGGCAGTGGTGACTTTCTAG GCAGGGAAGTGGTTACATTTTGTATTT GAAGGTGAAGAGTCGTGACATTCTGGGA AATAGGCAAGATGGCCGTTTCCCCTCAG CTACAACCAGCCATGCAGACCTCCTTGC AGGGACCTGGCTATCTACACTGGAACCA GAAAGGCACGCCCTGCTTTAGCCTCAGG CAGAACGATAATAACAGCGTGCTAGCTC AGTAGTCTGTGTGCTGGAAGGGTTTATG AGGAGGAAGTCCGCAATTACATATTTCT GGGCAAACATTAACCAAGATTGAAACCT AGATTTGAAGAGAAGTAGCAGGCTGGGA TC	p000687	D	--



SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
36	IM000654	AGATGAACCTATAAATGCATCTGCAGTCC TCAAATAAAGATGAATAGTAACCCAGAG GCGTGGTAGTGCGCTCTTCAAACCCAGT GCTCAGAAGGTGCAAACAAAAGGACCG GGAGTCCAAGGCTAGCCTTGACTAGAAG GGGCCATGTCTCAAAGAACAACAACCAA GAGCTGCTTATGGAGGTCAGTCTGTGTT CCCAGGGGGACAGCATCAGTCTAAGTTG GCGGTTGTTGTTGGCTGAGCATGCACAA ATCCCTAACAGCACATAAAGCAAGTTGT GTCACACACTCACAGTGCCCAGATTCAC TGGATC	p000688	B	Mm.1313 36
37	IM000655	GTCCATTGTGTAAGTGTGAGAGAGGAGTTAG GTTTAGAAAGCCTTCCTCAGATGTCCCT CAAAGAAGCTGCTACAACTGCCCTCATC CCACGTTGCCAAGGATC	p000689	D	--
38	IM000656	AGCTGTAGGGAAGCCCAAAGCACAGAC GACTGCTGCTGCTGCTGCGGTTCCCACT CTGGGTTGACCTTAGAAACGGGGTTCA TCTCCTCCAGCAGCTCCGGAAGGAAG GTGAAGGGGACTAACCATGATGAGCTTT GCACACTGGAAGTCAAGGCTGAGAAGG GGCTGGAGGGAGGCAGGGAAGACATCC CTCACGGTAGTGTTACACAGCTGGCGTT GCGGGCTGCCAGGGTACTCATTTGAGTC CATGCTGAGTCTCTCGGTGCCTCCTGAG ATC	p000694	K	Gfi1
39	IM000657	GATCGCCCCAGTTACCTCAAATTGTGTG AGTGTGTGTGTGTGTGTATGCATATAT GCATACAAGCATATACATGCATGCATATA TATAATACACATAGACATATATACACACA TATAGACGCATACATGCATTTGTATGCAT GCATCTATGTATGTACATATCCACAACCA AATATACCAAACACGCAGACACAGCACA CATAGGACAATAGTAATTGTGAATCTAAC TGGTGGGGTTTATGGGTCAAGAGCCAG GGTAGAGGAACTGGCTAAGGCTCTAAC CATCCTAGAGCAGGCACATCTACCAGGA AAAGAAACAAGGAAAAGAGCAGAGTTGA GGGTTACTTAACATG	p000695	D	--
40	IM000658	ACAGAATCTGTGGGTCATTATTACGTTTA TAGGAACAGGATTTTCTTTCTTTCTGAC TCTACCTTCTAGAAAGGCCGACTTTTAAA TCCTCATGCTCTTGTCTATTGACAGGAAA AGATGGGCTTCCCACTGATC	p000700	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
41	IM000659	GATCAGGCTGGCCTTGAACACACAGAGA CCCACCTGCCTCTGCCTCCTGCATGCTG GGATTAAAGGTGTGTGCCACCACTGCCC AGCTCACAAAGTAGTAGTAGGACTAGTA CTAGTACTAATAATAACAAACATTACAAC AATCTTAATTATTTTTGTTTCTACCTTTAA AATCTCCCAACTGTCTTTTATATTGCCT CAAGTCTTCCCTCAGTCCCTGGCCTTCA TAGCTTGACTTTTTTGCTAGAGGTTATCA GTGGCTCATCTCTCCTGAGATTGAGC TGGCTAAGACCACTATTCAGAGGGAGAA TGTAATGTCTCAGACATCATAGCCAGTC CTCAGTTCTCCTTTTGCTGACTGACCACT TTGCCAAACTAGTTTTCTAAGCCATACC TTTTCTTTTAAAAAATAGTCTTTCTTATA GTGGGTGCTGGCTTTGAACCTCTGTCCT CTTGCCTCACCTTGCCTGGTAGTAGAG GCTTGCAATTTACCG	p000702	C	--
42	IM000660	GATCAAGAACGAAACCCCTGAAAACATA AAACAGTAAGATAACAATAGCGTGCCTG ATTTTGTCCAAACCTTCTTGTCACCTGTC ACTGAGATTGTCAACTCCTTTTACCACC CTACATACGTTAGTTAGCTCAGTTTACGA GAGTTTGCAAAGGCCCCCACCAGTACCC TGCAACTTTACCCACCCCTGCATGGGAC TGTGAGAAAATGGGACTGGAGAGTAACC CTCTTCAGGCTCACAATCTGAGCTAGTC AGAGCATCTCACGGGTCCCGGACTTTC AGTGTGCTTTCCTCTTGGGTATTGGA TAAACAATGTGTACCGATATGGGTGAATA ATACAACATCCATGGAGAAATAAGCCAA ATCAAGACACTTCTTCAGAGG	p000703	D	--
43	IM000661	GATCAAAAACATCAACGTAAGGAGCCCT TAATGACGCTTTGTGACGTTTAGAATG GTCTACCCAAACCTAGCCAAGTCTAACT ATGTTATGGAGGTGGTAAAAGCAGTTAA CCTAAACATCTGGGACACTCACAGAATG ATAGGTAGGTAGGTAGATAGATAGATAG ATAGATAGATAGATAGATAGACAGACAG ACAGACAGATGTTGAATAAAAAAGTGACG TTTACAGTGATGTTAGCTCAAGGCAGGG CTTTTCAGGCCATTTCCCCTGGTCTCAC CC	p000704	D	--
44	IM000662	CTACTAAGTCCAGAGCAGAGAAGGAGGC GCCGCCTGTGTGCACAGCGGAGTCTGG GAGAGACCACCGGCCCAAACAGTAAAC ACAGGGCACCCACCGTGCTCCGATC	p000706	D	--

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45	IM000663	ACAGTAATCTGATTATCTTGCAGTAGATA ATTTGTCTACCTGTTAATGACTCTGCTTC TTGAACTACGTCCCAGTAGATGCCATGC TTTCAGCCTGGTAAGTGACACTAATACTA CCTCCAAACTGTCACCTTGGATTGTCAGG GTTTTGGTGTGGTGATGATACAGGAGAA ATGTAAACACGGAGTTGATGATAGAAA GGAGTCACTAATACATTTTCTTAGGAAAA GTCAAGTGACACACAGCAGAATCTAGCT GAAGGAGCTCCGCCAATAGGGCTGGAA GATAACTCTCGCACTAACCTGCTTTATTA GGAAGTGTAGGAAAGGCAGGTCTGCAG CACAGTTGAAGTTTAGGTTGCTGAGAAA GTTTCTGCTCATATTTATTACCAGTGAT GATC	p000708	D	--
46	IM000664	GTTTAGCAAGTCCGAGCGTGTTGATC	p000709	K	<i>Nmyc</i>
47	IM000665	AGGCAAACCCATGTGAGGCCTTCTCACA TCTTTCCTTGGATGCCTGCACACACCTG ACTTGACAGACTTCAAATCAGACTTATCA ACTCACCTCTTCAGTCCTGGGCCTCTTC CTGTATTTCAATCTTAGATAGAAAATTGG TTCCACTGTCTACCAGCCTTGAACCAGG AATGCAGAGCCAACCACCCCTGGGGTGT CCCAGGCAGCTGGGCTGGATGCTACCT GTCATGCTCTTGATC	p000710	C	--
48	IM000666	ATGTATGAGTGTGGGGCTGGGTTTGAAC CTGTGTCACCTTAGGACTCTCTGAACCT CGGTTTCCTATTAGACGGAGGGGCTATT CGGAGTCCTCATCTAATGGAGACACTTT GTGGGTATCAGAGGGCAACACTGTGGTA TTGGGGGTGGGGGGTTGCTGCTTAGAG CTCAGAGAAGAGGAGTTTGGCTTGCTCT ACAGAACATGCAGGCTGAGGTGTGGGT GCAGGGTTTCCCTGAGGCCCGGCTCT GACCTCTCCCCACTCCATTTCTGCGC AGGTGAGCGACAAACGTTCCAACAGCTT CCGCCAGGCCATCCTTCAGGGAACCG CAGGCTGAGCAGCAAGGCCCTGCTGGA GGAGAAGGGGCTGAGCCTCTCTCAGCG GCTCATCCGCCACGTGGCCTACGAGACT CTGCCCCGGGAGATTGACCGCAAGTGG TACTATGACAGCTACACCTGCTGCCTCC GCCCCGTTTCATGATC	p000711	C	--

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49	IM000667	GATCATTTTTCTCTCGAGATGGATTAAAG CTATGCTGCAGAAGGACCCGTGTGTGTC CTGTGTGTGTGTGTCCTCGCCGGCGAGA CTCCTTATCACACATGACAGCTTCAAAGC CCCCAGATTCAATAGGTTCCAGGAGTTC ACATTTAACACTCATGGGGTCAAAGTGC AGGCAGATGGTGGAGCCTGTGGAAGGT CATCAGACAAACAACCTGGTGGTTGCAG CAGAAATCACCAGGCAAGTAG	p000712	R	--
50	IM000668	GATCTGGCTAGCAGGGAGCCATTTACAG CTCAGACATCTATCATCCTTA	p000713	D	--
51	IM000669	GATCATTGTACCTCACCTGTCAGTTTGAC AGGTGGGAGGTGATATCTTTTTCAATTCA TGTATTCTTTGAAAGTTTGTTTCATGCATA TAATACATTCTGGTTCAATTCACCACTCC ACCCTTTTGTATCCCCTGCGTACCGAGC CCCCATTTTCTACCAAGTCTTACTGTTA TCTCAGTTTTGGGGCTTAGTTTTTTGTTT GTCTTGTTTTGTTGTTTTTGAACAGGGT CCCGTTATGCAGCCCTGGCCCTGAACTT GCTAAATAAACAGGTTGGCTTTGAATTC AGAGTTCTGCACACCTCTGTTACCCAAG TGCTCAGATTAAAGGCGTATACTACCAC	p000714	C	--
52	IM000670	GATCAATTCAATCTATTGCAATAACCTGG TTTTTTTTTCCGCAACTCCAAGATGGGG GGGGGGGGGCCAGTCAGGAGAGGTTT CAACACAAACGCACTAGTATTTACACACA GAATCTCCTCCACTGTTCTTCTTTGC TTTAAAAGTCTTTGTTCCGGAATCTATAG ATAGGGAGACAGATGGCTAGCTCCCCAA GGCTGAGAGCAGAGGAGAGTATAACA GGGAAGTCAAGGGTCTGGGAGGGCAA GGTAAGGAAGCCACAG	p000715	D	--
53	IM000671	CAATGCCTTCCCCGCGAGATGGAGTGG CTGTTTATCCCTAAGTGGCTCTCCAAGTA TACGTGGCAGTGAGTTGCCGAGCAATTT TAATAAAATCCAGACATCGTTTTTCCTG CATAGACCTCATCTGCGGTTGATC	p000716	K	Myc
54	IM000672	TAGTATTCAGGAAAAAGGAACTGGGAA ATTAATGTATAAATTAATCAGCTTTTAA TTAGCTTAACACACACATACGAAGGCAA AAATGTAACGTTACTTTGATC	p000718	K	Myc
55	IM000673	GATCAGAAAAACAGCCCATTATTCAAGAT TCAGGT	p000719	D	--

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56	IM000674	TAAC TTCAATTTAATAATTATCACATGCTA GGA ACTAAAGAGGTGCACAAAACAAACC AACAGTGGTTCCTATCCTGTCTAACAGAA GAAACTACAATTGTGGTTTGGGATGCCA CATAAATGACAGCAACGGGACCTACAGA AAATTAAGTCACAGAGAGAATGGACCAT TTCTGCAGAGACCTGGAAAACAGACAAG GGAAGAAACATGGTGTGTCTAAGTGATG GGGCAGGTGGTGCAAACGCTAGAGGCA AGCAGAGGGGATATGAACTGTGCTGCA CAGCTGGACAGAAGGGAGGCTGGAAGG GAAGAGAGGACCCTCTGTTTTGACTCAA TGGCTAGATGCCATGTGCCAAATAAGAA AGCACTTGGGGGGTCTGTGGGAAATCG GAACAGAGGGACTGGAATCAAACCTCAA CGTTCCTTGCATACTCCAGATAAGAACC AGGCTTTGAGCCAGGGCCTGGGAAGAG GGCTGGCCTACATATCTCATTTTAGAGAT GAGCAAACAGGACTGGGAGCTCTAGGT CTTCAGTGACACGCTTGCTTGGCCCGCA GGAGACCCTGGGTTTGATC	p000720	D	--
57	IM000675	GATCATGT CATGGGTCAACAGAAATAATT CTGAAAGGCTAAGTCATTCTTCTACCCC CAAGAAAAATCAAGAACACCCACATTA CAAACCTTCCGTAGTAACTGAGAATGG AGCCATGGCCAGAGCCCCTCTGCTCTCC CATCCCCCAACCAAGAACCAAAC	p000721	D	--
58	IM000676	ATATAACTTCTTTTTTTTTAAAAAGAATT ATTTATTTTATGTATATAAGTTCCTTATAG CTGTATT CAGAGACGCCAGAAGAGAGCA TCTGATC	p000722	R	--
59	IM000677	GATCATAGCACACTGGGGTGCCATCTGT CACCCCTAGACAAACATCTTTAACCNCG ATCTCTTCCTGAAGCCCACTTGGACCAC CCTTTGGAAAACCATCACCAAGGCCAGT AAGGTACCCGTGGTGACTCACCTCAGCC TAGCCCACCATAGACGCTTAGCAGAGCA GGTGTGTGTAAGTCAGAGCCAGACAATC AGAACACTCTCCCTGCTCCAAAGTAGCA ATGTAAAAAATTGAACCCAAAGTTG	p000724	D	--

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60	IM000678	GATCAAAGTAACGTTACATTTTTGCCTTC GTATGTGTGTGCTAAGCTAATTAAGAGCT GATTTTAATTTATACATTAATTTCCAGTT TCCTTTTTCCTGAATACTACGCTGTGCAT TCTGTACAATCCCCAAACGTATACATACA CACTTTATATATACACGATAATCTAGCTT ATTAACCAACCAGAAACATGAGTCTTTTG CTCTGTGCATTGGTTCTAGATTTATTATA TAATGCATATTCCTCGGGATTGCTTAT CC	p000727	K	<i>Myc</i>
61	IM000679	GATCATTGATGCTTCAGATAAATATGTA AATGGTGAC	p000728	B	<i>Mm.1278 81</i>
62	IM000680	GATCAAGATAATCCCCACAGGCATGCC CAGAGGCCCATTTCTAGGTGAGACTAT AGTCTGTCAAGTTGACAATGCTAACCATT GCAGTGAGGGAGAGAAAGAAGGCCAGG ATGGTGCCTCTCTGTTACTCTGCTTACCC ACGGGGTGCAAGGACAGTGGGGGATGG GCCTGAGCTTCCTCATGAACACACACAT GAGAGCAGTCAGCACATGGCCTCTTCT CTAAGCTTCACAGTGGCAGCCGCACCTC TGCTGTTAAGACCTAACATGTGGCCGGG CAGTGGTGGCACACGCCTTTAATCCAG CACTCGGGAGGCAGAGGCAGGTGGATT TCTGAGTTCGAGGCCAGCCTGGTCTCCA GAGTGAGTTCAGGACAGCCAGGGGCTA CACAGAGAAACCCTGTCTTGAAAAACCA AAACCAAAACCAACCAACCAACCAACCA AACAAACCATCTAACATGTACATCCTATC CATGTGCACGAATCATAC	p000729	R	--
63	IM000681	AGACCAGTGCCGGAGCCGTTCTGGCT GAGGCAGCCCAAGTCCTTGAAGAGCTTG AAGAGGTCGCTGCCGAACCTTGACGCCG ATGAAGGCATACAAGAAAGGGTTGACGC AGCAGCGGACGGAGGCCAGGCTGTAGG TGACGTCATAGGCAATGTTGAGCTGCTT GCTGGTTTCGCAGCTGCTATTGGTGATG TTGAAGTTGGCCACCGTCTGAGCCAGGA CCACCCCATTTGAGGGCAGCTGGAAGAC TATGAAGACTACCACCACGGCAATGATC	p000730	A	<i>Cmkbr7</i>
64	IM000682	CCCTCTCAAGCCTTCCTTGTTACTTAGCC TCTATAGGTCTGTGCATTATACCATCATT CTTTTAATTTACAGCTAATATCCATTTATA TATGATTATGTACCATATTTGCCTTTTGG GGTCTGGATTGCCCTACTCAGGATGACC TTTTCTAGTTTGATC	p000731	D	--

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65	IM000683	GATCATGATGTTTGTGAAGCAACAGAAA CTATAAGACAGTGCCCAAGAGCCTCTCT GGAGATAGCC	p000732	D	--
66	IM000684	GATCGTGTTAGACACAAGTAAGAAATGA ATGAGTCTTCCTGATTTTTAAATTAAGTT CTCCCCATATTGGCTGTCACTACTTTTAA AATCAGAAAAGGAGAATCTGGACGGTTCC AGGCCTGCAGCGCCATGCTTGCAAAAG GTTTACAGAATCGCTCTGGACAACT	p000734	D	--
67	IM000685	CTACCACAGCATCTTTGAGTGTATATAG TCAGTGTGCTACATGTTATCTATGAACAT ATGCAAATGAGGTTTGAGAATTAAAGTTG CTGATAGACTCATGGGTTAGGGGTTTGA TTGCCTGCTAATGATC	p000735	D	--
68	IM000686	GATCACGAAACGGTTGACTAAAGCAAGA CTGAACCACAGGCAGATACCAAACCCAA AGCTCTATGTCTAGTGTCTAGAATACATA GGTTTGGGTAGCCATGCCCTGTGACCC TGCCACCTGCAGCACACATAAGACAATA CTATAGACAACCACTTCTGAGTCAGAATT GCAATGATGTCTTTGGCAAACACTCTAG TCTCCTTTGGCCAGGAGCTGCTAAGTGG TTCAGGCTGAGGTACAATCAACCTAGGT AGGTGGGACTGTGTGCCCTGTGCTCCT GGGTGGCCTTCATGTCTGCTATGCTTGC CCTTT	p000736	D	--

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69	IM000687	GATCATGTCAACTATACCTGGACACGGA CCTTCATCCTTGCTGGTTTCACTACCTCT GGCACCTGCAACATCTTGCAGTTTTTG GAACCCTGTGCATCTATCTCCTCACACT GGCAGGGAACCTGTTTCATCATTGTCTTG GTCCAGGCAGATTGAGGGCTGTCCACTC CCATGTACTTCTTTATCAGTGTCTCTCC TTCCTGGAACCTCTGGTATGTCAGCACCA CAGTGCCACCTTGCTGCATACCTTGCT CCATGGGCCTTCACCCATCCCCTCGTCT GCATGCTTTGTCCAGCTGTATGTCTTCCA CTCCTTGGGCATGACCGAGTGCTACCTG CTAGGTGTCATGGCTCTGGACCGCTACC TTGCTATCTGTCTGCTCCACTGCACTACCAT GCACTCATGAGCAGACAGGTACAGAAAC AGTTAGTTGGGGTTACATGGTTGGCTGG TTTTTCAGCTGCCTGGTGCCTGCAGGTC TCACTGCCTCTTTACCTTATTGTTTGA GAAGTGGCCCATTA	p000737	C	--
70	IM000688	CTGTCAATTCATCCAGCTCTAGGCCGCT GTCTGGCTCGATGCTTATTGGTTTAA GTGCCGATGCATAGGATTCTACAGTCAG AGTGGCCTAAGCAACAGCTAAATATTGTT TTCTTGCTGTTCTGGGAAGTAGATGTTCA AGGTCAAGGCGTCAGTAGCTCTGTTATG AGACCTCTCTGCTGTCGGGCTGTGTCTT CAAGTTTTTCCCCCTCTGTGCATGTGT GTTCTATTTCTCTGCATGAAAGACCAG TAGAGCCAAGTGGTGGCACACACCTTTG ATC	p000738	D	--
71	IM000689	GATCATGAGAGGCGAGAAACCCAGACAT CTCTAACTCTTCTTGCCAACTCAGGAGC CACCTGTGGCCCCAGCTGGCCACCAGC CGTTCTCCCTCAGAGGCCTCCATTTCC ACAAAAGGCCTTCCTGGTTGTTTCAGGAC AGAGCCTGGTTCCCTGATACCCCTTCT CTCAGTGGCCACTGAAGTTACAGGGATG CAGCCAGCCGTGGTTGCCATGTCTGTAT ATGCTAATCTCCGAATTCACCTTCCTGTT TAGATTCTCAG	p000739	D	--
72	IM000690	GTTTGTCCGCATGAGTCCCAGGGACCAC TCAGAGTGGCTGGCAGGCATTGTGGAGT GGAATGTGGGAAGACACATTCCCAGCCT TGTTTGCAGCTTGGGACTGTCTGTGTTT GGGATGATC	p000740	D	--



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73	IM000691	GATCACCTGGGAAGGGGGAAAAGGACA AGTCTGAGCTCCCAGCCCACATTCTCCT AGGGTAGCAGCTCCCTCACTTAGTGT	p000741	D	--
74	IM000692	GATCAGTTCTTATTAACAATACAGACTT AGGCAAAATGAGTCAGAAATAAGGATAT CGCATATCCCGAGACCATTGAACTCTA AGAAGTATTTTCTATTATTAAGTAGTTCA CCAGGCAGTGGTGGCACACACCTTTAAT CCCAGCACTCGGGAGGCAGAGGCAGGT GGATTTCTCAGTTTGAGGCCAGCCTGGT CTACAGAGTGAGTTCCAGGACAGCCAGG GCTACACAGAGAAACCCTGTCTGGACAA ACCAAAAAAAAAAAAAAAAAAAAAAG	p000744	R	--
75	IM000693	GATCATCACAGATGACATAGAACCAAAC TGTAACTTTCTAGACTACATGTAGCAGAC ATTT	p000745	D	--
76	IM000694	GATCATACATGAATACAAGCAGGCTTCT GGTATACTCTTAAGTTGAATTCTGTTTTC TGTAGTCGTAGTCTTGCTTTTCCAGTTT TAAATTCTAGAACAGGTATACTGTAGAGC ACCCGCCTCCCTTGCTCTGGAGGTAGG GTAGAGTGGGAGTTAAGGTCAGTTCC	p000746	B	AA65702 8
77	IM000695	ATTTCTCTTGTAAACTCACTTTCTGTTCA CCCATTTTGTCTGTGTCCTTACTAAATTA TTTCTATATAGGAATCTTTGTATCTTCTGA TATAAGCTAGCGCATGGGTACCACCAGC ACCCAAGTCATCTGCTGAGGTGCTTCTA ACCTTGCTTGATTGAGTGCTTCAACAGA AGGTGGAGTAAACAGGTCATTTTTTACC CTAGAGAGTTCAGATC	p000748	D	--
78	IM000696	GATCTCCGGGTGCCAGACTTGCCCAGCA AGCACTCTTACCTGCTGAGCCATCCTGA GGGCCTGGATTTAAAAAAAAAAAAATATTG ACATATTGTTT	p000749	D	--

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79	IM000697	GATCTCCTAAAACTCCCTGTGTCAGGAA ACTTTCTGTGCTTTTGTATTGCGTTCCTG TGTTTCGTGGAAGGCCCCACGCCCTTCAT CCTTGCTAATTCTTTTTGGATAGCTTGTT GCTTTAACTAGATTGGCCCTTTCTTGGCT AGTATTTTCTGCTGTACCTATGAGTGGTG TGGGAGAACTGTGCAGACTTCCAGGAAG CGCAGCCATGAAGCTACATGTGCCTATG TGTAGACACATCATGGATTTTCTTACTAG TTTACTAGTGGGTGATAATCTGTCCTTTT GAGCTCTCCAGAACGTTCTAGAAGCTTA AGGAGAGAAATCACTTAAGAGAG	p000752	D	--
80	IM000698	ATCTGATAGTAAGTAAAAGGACAGCTAAA GATGAAGGGAAAGCAGGAGAGTCCTGG AAGAAGAACTAGTGTTCCTAAGAGTTCA TCATTGATAAAATGCAAAAGAAGTCAATT ACATACATGTTTAGGAACTGAATCCTCT TGTTTTGGGGGATGTTTGTTTGAGGCA AAGGCTCTCTTACAGAGCCCTGGCTGTT CTGGAGTTCTGTATATCAGGCTCTGGCC TCAAACCAAGAGATC	p000753	D	--
81	IM000699	ACATCAAGAGGAAGTTGGAAATGTCATC TTTAGCTATCTTATATCCTGGTAGCTTTA AGATTTCTTTGTGTGACTTTATAGTTCT CAAAATATTTTAAGGGTCAGGGGAGGA AGCACTTTCAAGAAATGAGATGGGAGAG GGAATGTCTTTGTGTTGCCTGGAGATC	p000755	D	--
82	IM000700	AGCTATACCTGAAATTTGGCCAAGAACA GAAGCTCAGGAAATAGTGTGATTTAAAAA CCAAAACCAATTTACAAAAGGAAGACTGT GGTGTAGATC	p000756	D	--
83	IM000701	CCACAACCTGAAAGCAACACACACAGTAT TTTTCTGTGGGTTTTAGGATGTATCCACA CTCCCGAACTTCCTTTCCCTGAAGCACC CCTCAGTTTACTCTGAAGCATGGTTTGA GTCCAAGGCCAGTGTCAACTTTCTGCC AAGTCTCAATGGCAAAAGTCTGTTTAAAT CTGCTCAGGCTAATGTAGATC	p000757	D	--

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84	IM000702	CTTCCAGTCTTTTATGCTATTTATTGATAT GAATTCCTGCCTTATGTATCATCCAAGA TTCTACCTAAAATACTTCCAATAAGTATC AAGGACCACTCAAATATTCACTATTGGAC TTAGAAGCTCCACTCTTAAAAATAGATTCT TATAGAAAGAGCCTGAAATGGGGGCATG AAATGGGTCCATCTCCACCATCACGCAC ACATGAACAAAGAAAAGGAGGAAATGGT GTTAAGAAAACCTTACATCATACTATTTAA AAATAAGGAGGAAGGAGGGAGGGAGAG AAAGAGAGAAAAGCTCAATGCTTAGGCAA GAGTGCTTAAGAAAATTACAGTTAACAGATC	p000758	D	--
85	IM000703	GATCTCCTAAACTCCCTGTGTCAGGAA ACTTTCTGTGCTTTTGTATTGCGTTCCTG TGTTCTGGAAGGCCCCACGCCTTCAT CCTTGCTAATTCTTTTGGATAGCTTGTT GCTTTAACTAGATTGGCCCTTTCTTGGCT AGTATTTTCTGCTGTACCTATGAGTGGTG TGGGAGAACTGTGCAGACTTCAGGAAG CGCAGCCATGAAGCTACATGTGCCTATGT	p000759	D	--
86	IM000704	GATCTGAGTGCTGGGAACCAAACCTGGG TCCTCTGCAACAGTTTGTGCTCTTAGCTG CCGAGCTTT	p000760	R	--
87	IM000705	GTACGGCGATGGGCACAGGCTTCGGGA CAGTCCGCGCGACGCTCAGGCGGACAA CGGGAGGCGGGCGGGGAAGGCAGGGG CTGCAGTGTCAAGTCCCTGACCCGGGA GGCTCGGAAACTTCACTGCCTCTGCGCA TCCGGCATGGCCCCTCCCACTCGGACTT CGTCAAAAAACCGCCACCGTGGAGTGTC CCAGTATGTGCGGTGTGGGACAACTAT CGCACTGTTGCCCTGGCTCTTCTCCTAG ACCCCTTTGTGAGCCAAAAGAGAAACG CTGGGCAGATC	p000761	B	Mm.2739 3
88	IM000706	GATCTCGTTACGGATGGTTGTGAGCCAC CATGTGGTTGCTGGGATAA	p000762	R	--

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89	IM000707	CTGGGTTGACCTTAGAAAACGGGAGTTCA TCTCCTCCAGCAGCTCCGGAAGGAAG GTGAAGGGGACTAACCATGATGAGCTTT GCACACTGGAAGCTCAGGGCCTGAGAAGG GGCTGGAGGGAGGCAGGGAAGACATCC CTCACGGTAGTGTTACACAGCTGGTGTT GCGGGCTGCCAGGGTACTCATTTGAGTC CATGCTGAGTCTCTCGGTGCCTCCTGAG ATC	p000763	K	<i>Gfi1</i>
90	IM000708	GATCTCAGGAGGCACCGAGAGACTCAG CATGGACTCAAATGAGTACCCTGGCAGC CCGCAACACCAGCTGCGTAACACTACCG TGAGGGATGTCTTCCCTGCCTCCCTCCA GCCCCTTCTCAGGCCCTGAGTCCAGTGT GCAAAGCTCATCATGGTTAGTCCCCTTC ACCTTCCTTCCCGAGCTGCTGGAGGAG ATGAACTCCCGTTTCTAAGGTCAACCCA GAGTGGGAACCGCAGCAGCAGCAGCAG TCGTCTGTGCTTTGGGCTTCCCTA	p000764	K	<i>Gfi1</i>
91	IM000709	GGAAGAAGTGTGTGCAGGCCATGGTCAA GTCCTGCATGGCTCCCATCTGGGTCCAG CAGCAGCCAGCCTCCAGTGCTTGCTCCT GATGTCCCAGTGAAGTCAAGTCTGAGC AGCAAATCCCAGGGGCCAGTCCTAGGG AGAAAAAGAACACACTGCCATCTCAGTG CCTCAACAGAAAGCAAACCTAGGCGTCAG GTCATGTCCTTGTTACCCACATCACACCT AGACTTCCCTGGGTATCATGCTCTGTGT GAGATC	p000765	B	<i>Mm.1535</i> 12
92	IM000710	GATCTAAGGATATATCATTCCTAGGAGAA AATGAATATTTATGACCTTGGATTTGTCA ATGTTTTTTTAAATATGGCATTAAAGCCAC AGAGATAAAAATAAGAAAATAGATACATC GAATTCAGTAAATGAGGAAGTTCTTGT GATTCAACAGAAAC	p000766	A	<i>Mtm1</i>
93	IM000711	GAGGTAAGTCTGTTCAAGTGTAGCTATCC TTAGCAGCTAACAGTCCTCAAACTTTTT AGAGATC	p000767	D	--
94	IM000712	CTACAGATGCATTATTAATATTACTTTTTA AAAAAACCCAGTATACTGCTTGAAAACAG TGAATGCAATGGGTTCTCATTACCTTCC TGCTCTCAATCAATCTCCATCTCTAAAGC AAGAAGTGGGGGCCCTTCTGGCTGAGC GAGGGGTGAAGGGAGGGGAAGAGATC	p000768	D	--

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95	IM000713	GATCTGGAGAAGATGTCAAGTTTTAAAT GAGGCAG	p000769	D	--
96	IM000714	GAGTGAAGCAAGAATTTGGAGCCCAGCT GCCGCAGCCTTTTTCTTTTCAGCAAAGC TCGGGAGTGATAGATATGCATGAACCAA AGCAAAGCCTTGAGAGTGCCACTTGGCC CTGCCTCCTGAGGGTCTCAGGGCATCAG CTGGAGACCACCCTGTGACCCACACATC ACCGACTATGAAAACAGCTCATCAGAGT AATAAAGATC	p000770	D	--
97	IM000715	CAATGAACAGGACACATGCTTCACACGA CAGTCCAAAAATGCAAAGTGTGGAAGAA TTCCACAGCCATAGCCTTCATTACTAGAT C	p000771	D	--
98	IM000716	ATGCCTTCCTGGTAGAAGAGGGCCATGC TGTGGCGGGGAGGGGCCACTCAATTTTT CCTGCTCCCTTTCCCTGTCCCATATTCTC AGGAGCTTCTAGAAGCGTAGCCTGCATC TCATGCCCTGACTTGGCACCAAATGCTT GCTTTGTATCAACACCGCTTTCTCTTCTG CTCTTCCAGCTCGCAGCCATTCAAATAA TACCACCCGGTACCCGTGGAATCAGGAG CAGAGATTCCAAATTGAGTCCTAAATCA AATCCAAATGGGCCCGTCAGCTAGATC	p000773	D	--
99	IM000717	AGGCGAGCGGATTACTAAGGACTGAAAG ACTCCTAAGACTTGTCTCCTGCTCCCTG GCCAGCGGTGGAGCTCAAGCAGAATTG CAAGCTCAGCTCAGGTCTCAGTGATGCA AAGCACCCCTCGTTACTCCAATGTGTGTTA CTCCTACAGGTGGGCTGCCTTCCACTTT CAAACACCCGCACAAACAGACCTCCAC CGTATGCCAGAGCATCTGTTTCGATGCTT TCTGGAACTATGCAAGCCCAAATTTAAT ATCCAATCAGATC	p000774	D	--
100	IM000718	GTGTGTGTGTGTGTGTGTGTGTGTGT GTGTGTTACAAGGTCTCATACAGAATCC AGGCTGGTCTCAAACACTGGAGTCAAG CCATCTTCTACCTGGCTTAGCTGGGGT CACAGACTTGTGCCATCATGCCCAATGG AATGCTGTTCTTTTGGAAAGCCTGCTAC TGTCATATACTGTCATAGGAGTTAGCGA CTGCTGGCTTATTCCTTCGCTTTGCTTGG AGATC	p000776	R	--

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101	IM000719	CCCCCTTCCTGTACCTCCTGACCCCTT GCGCAAAGGAGGCTCGTGGCCCCGCTGT CCCACTGGGGGATGGGGCTGGGGTTGA GAAGGCTAGTGAGCGCCTCTAACGCTCA GGAAGTGAAGTTTGTGGTTTTGGGGGCT GAGCTCCGAAGGAGATTAAAAAAAAAA AAAAAAGTCAGAGAGACAGATC	p000777	D	--
102	IM000720	CTTTGTATAAGCAGCAAACAAAAAGCCA GAGGCAGTCCACAGATC	p000778	D	--
103	IM000721	ATACAACAGGAGCAAAGCTGGAGGGGA ACAGATATAGAGGACAGTTCAGGGCATC TGCAGAGGTGCTGTGGAATGGGGAGGG GACAGTGGATAAGGGGACTTACCCTGAG CATCTCGGTAATAAGCATGGGTCACACT GCGGAAGCGCTCCTGTCTGCAGTGT CCAGATC	p000780	A	Rab37
104	IM000722	GATCTATGTCATCTTCCAGGACTCAGAG TTAAGAGAGTTACCAAGTGAGAGCTCTC ATCACCTTCTGAAGCAGTTGAGAATTGG AACCCAGAAAGATGCACATGCACGGGCA CACACACACCCACGGGCACACACCCAC CCACCCATGCAGAGAGAGAGAGAGAGA GAGAGAGAGAGAGAACTCACACTGGTAC TGCAGTAAACGGGAGCTTGTTT	p000781	D	--
105	IM000723	GATCTTCTTTCTCTGCTCAATTAGTTCAC TTCTGCTTTCATCTCCTTTTCTTTGATAA ACCATGAGTTTCATTAGGGCTATTACAAT CACATGCAGTTTTTCTTATAGTA	p000782	D	--
106	IM000724	GAATTAGGCCTAGAAACATTAGAATCCA GACCACGGAGCTCCCCAGATC	p000783	D	--
107	IM000725	GATCTTGTTCTAGAACGACCCTGAAGGC AGCAGAACAGAGCAGGACTGAAGGCCA CCAAGGGGATTTCAACTCTTCAGAAAAA ATAAGTGACTCACCTTCTCACAAAGAGC AAGAATCACAGAGGTCAGATTGTCTCCT CCTGCCCATCAGGGACAGAGTCCCCCAT CTTTGCCTTGCTCCATCTGGCAGGTAAG AGATGGGAAGTCTCCTTCCCTCGGTCT GCAGCATCCCTGGCATCCCTGGGGAGT GTTGGCACAGAACCCCCCTCCCAA	p000784	C	--
108	IM000726	GATCTGTGTGGGCAAAGCCCATGTGCTG CAGTGTGTCTGGGTAGAAATGAGTTGTG TGGTGCTCAAATGTAAATGAAGTCCCTG TGTT	p000785	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
109	IM000727	GATCTCATTACAGATGGATGTGAGCCAC CATGTGGTTGCTGGGAATTGAACTCAGG ACCTTTGGAAGAGCAGTCAGTGCCCTTA ACTGCTGAGCCATCTCTCCAGCCCCCA CCTTTTTTTTTTAAAAGATTATTTTATAGT TTTTGCTTTTTTAACAGTACTGGAACATC TCAGTAATTGCTAAGTTGTCCTTGCTCCA GGTGAGCAGTCATATTTCTCCAATTCTG GTTTCCTTACTTGTGTCAGAGACCAAAAT AGCTTGTTAATCAGTTAGAGCTCTTTAG TTACCCATATCTGTGTAGTAA	p000787	R	--
110	IM000728	TAAGAACATAAAAGCAAAATTTGGAGGCT CAAGATTCAGTTTAGTTGCTAGAGGGCT CACATAGCATGCCCTCCCCACCCGGGAT TCCATTCTCATTTATCGAGGCATAAGGCC AGGTGTGGTGGGATATGTGCTGGGATG CATAAGATC	p000788	D	--
111	IM000729	GAAAGGCACACTGGTGAAGGCTGAGGA CCACCAAAGCTGCATTTCTGCTAGGCTA GGTAGAACAAGAATGGTGCTCCACTAAG AACTCAAAAAGCCACAGCCCACCCCTGA GGCCCTCCATCTGACACATGCCGGTCAC CTGTCCTCCCACAGCCCAGCACAGAGAA GCCACCATCCCTCCCCTTCCCACCTCCT GCAGCTGACAGTGTGCATCTTTCCGCAC ATTCCTCTCTCCTCAATCAGGTCAGAATG TATCCAAAGATC	p000789	D	--
112	IM000730	CACTGAAAATGGCTAGAATTCTGGTGAT GGGTGAGCCGATC	p000793	D	--
113	IM000731	GATCGGAGTCCCTCGTTTCAGAGGCCCC ACTTCTATGGCTCCTGCCTTCCTTGGCTA CATCCATTCTGCTGAGTCTCCTGGAAAC CTGTGTATCAAGTCTTTTCCAGTTAGTGC GTTCTGAGTGGCTCTAGAAACCGCTTCC CATTACAGCGAAAGACCCGTATAAACCA TGTTCTCTTCTCTGTGACAAGAGACAAC AGACACCGCACAAAGGACTGTCTGGCCT GGGGGGGGTCCCTGGTTCACAGCTTC AGTCCTGA	p000794	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
114	IM000732	GATCGCTCAATATAACAGCAACATGCCA AGTGCCACTTGTAAAATTTGTTGTTGAGC AGTCTCATTATCAACTGAAGCACAAATGTC AGGCTAGCAAGAGGCAGGTTTCAGTTGTT GATTAGCGATAGCACACACAAGCCAGCA CATGCTTTTTCTGTGAGTTCTAT	p000795	D	--
115	IM000733	GATCGCTGAGTTTGTTTACAGAGCAGGG ACGCCTCAGCTCGGATGCCAAAGCTACC AAGAGCTGCAAACGCAAACCTTAGCAGAA GCACACGTACTCCC	p000796	A	<i>Cited2</i>
116	IM000734	GATCGCACAGGTAAAATGGGGACTCACT TTAGCTAAAACAACAACAACAAACAGCCT GATGAGTCGAAAGTCTCTTAGGTTGCC CTCTGTTCTCCAGCCCCACATCCTGAAG GCTGTGCATTCTCCACAGCAGTCTCA AAATAACCATAGTGCTCAAGTCCCCTGTA TCAAATGGTGGTATCTGCATCCACCCTA CAGGTGTTCTTTGATTCTTTCTTTCTTTG TAAGTGTGTCTGGGTGTTTGCCTGAGC GTATGTATGCGCCTAGTACCTGCAGAGG CCAGAATAAGGTGTCAG	p000797	D	--
117	IM000735	GATCGTGAGAGGCGAGAAACCCAGACAT CTCTAACCCCTTCTTGCCAACTCAGGAGC CACCTGTGGCCCCAGCTGGCCACCAGC CGTTCCTCCCTCAGAGGCCTCCATTTC ACAAAAGGCCTTCCTGGTTGTTTCAGGAC AGAGCCTGGTTTCCCTGATACCCCTTCT CTCAGTGGCCACTGAAGTTACAGGGATG CAGCCAGCCGTGGTTGCCATGTCTGTAT ATGCTAATCTCCGAATTCCACTTCCTGTT TAGATTCTCGG	p000798	D	--
118	IM000736	ACTGTCCGTGTGGGAAACGTTTAGCAAG TCCGAGCGTGTTTCGATC	p000799	K	<i>Nmyc</i>



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119	IM000737	ATTTCTTTTGGAGTACTTCATATAAGAGC TTCGCATCTACACCACTCTTGCTCGCCA CTCCTCTTTTCTTCTTTCATTAAGTACTGT CCACTCTCCAACTTCATAATCTCTCTAA TTACTATTGTTATTTACACACACACACAC ACACACACACACACACACACACACACGT ATATGTAACCTACTGAATCTTACTAAATA GCTTTACTATCTTCCAAGTAACAGGCACT TGATAAATCTTCTGTCAATCTCCCAGAAC AGAAGCCTTAAGAGTCATTTAAGTTCTTT TATCTCAGGCTGTTCTGTTCTATGCCTTT TGCTTTTAATCCATCACCGATC	p000801	D	--
120	IM000738	GAATGTCTAGATGGAGACTGGACAGAGT TGGATTCTAGACACCTAACAGAAGCGA AAGCAGGGGATGGATAAGGTGGGTGCC TCGTCCTACAGCAGGTTCTGAGTGTCGG CAGAGACTCCCATGGCTTGGCACCATGG TTGAAGCTTTCATCGATC	p000803	C	--
121	IM000739	CTATTTTCGTTCTCTCCGATC	p000804	D	--
122	IM000740	GATCCTCATGTCAAGGCAGGGGCAGAC CAGGGTCAAGGGAAAAACACCTGCTTTC CTGGGTTGTAAATGCCAGAAAGGGAAGG CACGGGGTGGGTAGGGTGGAGAACATG GCCCAGACCCCTGTCTCTTCTCT	p000806	D	--
123	IM000741	GCACCTGACTTCCTCATATAAGACACAAA CATCTTGAGTGCTGCGCAGGTGTACCAG GATACAGGTGAATCCAATCTGGTGGAGA TTTGCCCCTGCTGCCCTGATTAGCTGAA GCTGCGTGCCCTGGTGAGGTGGCATGGC CTGCTGTGCGTGGATGGGAAGTGAAGT ATAAAAGAGCGAGAGGCCCGGGTTAGA GGAGGATTATTATTCGAGAGAGGATTGT TATTATTGGGAGATATGAACAAGGGAGA TATAACAGGGGAGATATAACAAGGGA GATATATGGAGAAAGAAGAAACAGGACT GAATAAATGTGTGCAGAAGGATC	p000808	R	--
124	IM000742	GATCCTTCTCCTGTCTTCTTCTGGAAG GCTGGGCTACATGCCAACATGTCAGAGT TTTACCTGGGTTCTTCCAGAGGTTTGAA CTCAGGTCCTTGTAATTACACAGCAGCT ACTTTGCCTATTGAGTCAATATTTGTGT GTGTTTGTGTAGGTGTGTTTCATGTCTGTA TACTTG	p000809	D	--

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125	IM000743	GATCGTGCATGCATGGGTGTGTTTTGGG GAGAGGTTCTGTCCCTGCTAAG	p000811	D	--
126	IM000744	AGCTCAGCTTGTGAGGCCTGATTGTGAA CACTTCACCAACCGAGCCATCTCGTCAG CACAGCCCTGTTTTTATTCCCATTCT TTTCTGTATTTCTGTTGAATTTCTCACATA CTCTCCTTTCTCTTCTGCCTTCTTCTGGT TTCTGCATCATTTCTATATTGACATTTAAA CAACCCCCAAAATTCAAGATACATCAACA AAAATTTATTCAACTAGTCTTTCTTACTTC CATATCAATAATGAAAGAAAATTAACCC TTTCAAATTCAACAAATCCCTACACTACA TATAATCACTTTCCTCTATGCTAAATCCA ACTTGAAATTATACCTCAATACCCTGCT GGTATTTTACTGTCTACATCACTGCCTA GTCTTCGATC	p000812	D	--
127	IM000745	CTGGTATATGAACGAAGTTGGTCTCTAAA GGCCGTCTAGAACACGGTTCTCAACCC GAGGGTCGCACCGGGGTCACCTAAGAC TACTGGGAAAGCACAAATATTTACATTAC GACTCATAACAGTAGCAAAATTACAGTTA TGAAGTAGCAACAAAAAATAGTTTTATGG TTGGGGATTACCACAACATGAGGAACTG TATTCAAGGGTCGCAGCATTAGGAAGGT TGAGAACCACCGATC	p000815	R	--
128	IM000746	TTCTAACCTGCTAGGGTTTTCTCACGTG GGTTCTTCTTTGAGGGCTCTCTGGCTTC CCTACTGAGCTGTAGCTGCCAAAGTTGA AGGGCTGCGTCTCCCTTGCGTCTCCCCA GTCTTTACAGCTCCTGAAACACACTAAG GTATTTATTCAAATCCCTGTTTTGTGTGC GATC	p000819	D	--
129	IM000747	AGGGCCCTTCCACCTCTTCTAGAATTCTG GTAAGCTAAAAGTACATGTATCCGATTAA TCTGAAATAATTTGTAGACAGTTTGGTG ACGGGTGGAGGGTGTGTGGTTGCGCGA TC	p000820	C	--
130	IM000748	GATCGGCGAGACCACGATTCGGATGCAA CAGCAAAAGGCTTTATTGGATACACGGG TACCCGGGCGACTCAGTCTATCGGAGGA CTGGCGCGCCGAGTGTGGGGTTCGGAC CAA	p000823	R	--

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131	IM000749	TTGGCTGTGGAGATGAACGTGGGAACC GTGGAAATGACCCTAGAATGGGGCTCAA ATGTGAAAGGCATGCCAGAGGTTGCTCT GTTGTTTTAAGTCCCTGCCGAACATTAGA ATTTAGCCTCAGTTTTAAAGCTGTTACT GCCTAGTTGGGTGCTTCTTTCTTAAAAAG CAACCAAAAAAAAAAAGCCGTTTTCACT CTGAAATGTATTAGAAATTTGCATTAGCC CAATGGCTAATAAGCGATC	p000824	D	--
132	IM000750	GTTATAAGGATTGCATACAAATGGCATCA GGACTGGATGTGGTGGCACATGTCTTGT ATCACAGCACTTGGTGAACAGAGGCAGG GGAATCTCTTTGAGTTACAGGCTAGCCA GCATGACACGGTGAGACTCTGTCTTAAA CAAACAAACAAACAAACAAACAAAG GTAGCATAAGAGCGATC	p000825	D	--
133	IM000751	ACCTGAATCTTGAATAATGGGCTGTTTT CCGATC	p000827	D	--
134	IM000752	AACTAATACCTTTCCTTCCGCTGCGATGT TTCATGAGACTCTGGGTTAGTGCATGGT CAGGGGCCAGGCAACAGTGGCAGTT CTGCCCAGGATC	p000831	D	--
135	IM000753	GTTTAAAGAGCCGTTTCGACCCGCTTTC CGTTTCGCTCCGGGTCAGCTAGTACTGT GAACCGCTCGGTCCGGTCCGGCGCTGC TGCGCACCTACTCGCCGGGACCCTGAA GCCCCCAACTACATATAGGGGTCTTCC CGGAAAGTACGCAGGAAGTCGCGTTTCG GCCCCCTCCCCCAGCACACACCCAG TCCCTTCCACCCCCCGGGATC	p000832	D	--
136	IM000754	GATCCCAGTAGAGACAGAAACAGTGCCT TTGGTTAAGAATTCCAGGCAGGATGGTA CAGGATTGCAATCTCAGCATGGGAGACA GAGGCAGGATTTCCAGGCCAGCCTGGG CTACAGTATAAATGGGACCCTGTCTCAA GTAATTGAAAAAAAAACAGAGAAAGAATT TGGAGACTGTGACTATAGCTTGGTGATG GAGTCCGTTTGCCTAGCAGAGTGAAGCA GCTGTGCTCCTGTGTTACACCACAAAA TAA	p000833	D	--
137	IM000755	GATCCAGTGAATCTGGGCATTGTGAGTG TGTGACACAACCTTGCTCTATGTGCTGTTA GGGATTTGTGCATGCTCAGCCAACAACA ACCGCCAACCTTAGACTGATGCTGTCCCC CTGAGAACACAGACTGACAA	p000834	B	Mm.1313 36

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138	IM000756	GATCCTCCCTACCGGTCCTCGGGCAGAC CTCCAGCCCTTCCCCAGACACTGTTGGA AAGCAGGCACGCCTTCCACAGTATGGTC TGAGGTTAACCCATGACAGCACTCTGGG TGCCTGGTGGTGTTCCTGGTGGGGACG TCAGTAGCTGTAGCTCTGTCAATTGGTCC TTGCAGCGTCTCATTCCAACATTCTTCC CATCACTCCTCT	p000835	D	--
139	IM000757	ATATGTGTTTGTGCGTGTGTGTACATGTG CATGCATGGCATGTATGTACCCATATAAA TATGTGTATGTGTGTGAAGTGCTGATGTA TTTCACACAGCATTTTGGATTTAATGGAG AAGGTAGCTCAGATGTCAAGTGTGCCCT CCTGTCAGGAGAGGAAGCCTGATGTGC CTGCTGTCATAACTCTGGTTTTGATAAAT ACAGCACGAGTGATTTTGGCTGTTGGG TTTGCCGTGTATGGATC	p000837	D	--
140	IM000758	GTTTGCTTGCAACATTGTCATAGCTTAGT GAACAGTATAGCATTGTTCTGGCTCAAG AAGCCCTGGTCTTCAAAGCTCCTACTTA GATGAAATTATTTGCATCACAACAAAAA TTGTTTTGCATTTTTAGATAATGAAGGA TC	p000838	C	--
141	IM000759	GATCCTAGGCCAGTCAGGGCTACCAATA AGAACCTGCCACACACACAAAAGGAAAG CAAATTTTGCAAAACTCTAGTCTCATG GTGTCACGGTCTTTAAACATCTTGAGGG GCTCGAACTGGTGAGGTGGCTCGGAGG TAAAAGGGCTTTGATGCACAACCTGAGT TCAACCCCGTGTTTTAAAGACTTTCTGCA ATGATTCTGGTCTGCAGTCCTAGCCCAA GCACAGTCAAGGAGAGATTGAGGCTGAA ACGGAAGAATGGAAGTTGCATAACAGC TCAGTGGCAGAAATAACAGGAGAGACCT GACCTTAAAAACAGGGTGTAAAGGTGAGA AATGATGACAAATGACATCCACTTCAACT GTGCTACGAACAGCTACCTGTTTGCACA CCCCAAACACACACACACACACA	p000839	D	--
142	IM000760	GTAAGAGGGAATGTACTCTCTGCCATCG GGACACCCAGTGGAAGTGTACCTGGA GTCTTGCCCTCCACGAAGACTAGGATC	p000840	D	--

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143	IM000761	GGGACTTCAGGGCATAGAGCTTAGTTCC AGACAAAACCAAAGTTAGCAGTCGCCTC TCTCTTAAAGACGTTCTCTCTAGCCGCA GATGACCTCAGAAGGGGCTCTGGGAGC CGACTCCCACCCTTCCTTCTCTGTTTACA GAATCTGGTTGGGCTGTGAGGAGCGAC CCACGAGACGGGCTCCCTGTAGTGAGTT AGGCCAGTGGGAACCAACGAGGATC	p000842	D	--
144	IM000762	ACACACACTAACACACACTCACTCACAC ATACTCACACACTCACACACACTGTCA CACACACACACACACACACACACACACA CACACTTTTCCACCAGGATC	p000843	R	--
145	IM000763	GATCCCTGGATATGGCAGTCTCTACATG GTCCATCCTTTAGTCTCAGCTCCAACTT TGTCTCTGTAACCTTCCATGGGTGTTT TGTTCCCACTTCTAAGGAGGGGCATAGT GTCCACACTTCAGTCTTCATTTTCTTGA GTTTCATGTGTTTAGCAAATTGTATCTTA TATCTTGGGTATCCTAGGTTTTGGGCTAA TATCCAATTATCAGTGAGTACATATTGTG TGAGTTCCTTTGTTCAAATTTCAATTCAT CACCATTGTGTGTATATGTGTGTGTTGTG TGTGTATGTATATGACGTGTGTATGTTGT GTGTGTATATATAACGTGTGTATGTTGGG GGTCAAAGGCATGCTCATGCCACAGTGA ATGAGTAGACATCAGAGGACAACCTTCA GGACTCAGTTCTCTTGTCTACCCTGTG GTTCCAGGACACTAACCAGGTATCAG GCATGGTGACAAAGGTTTTGACTCAAGG AGCCATTTTACATGCCTCATAAGAAGGG CC	p000844	R	--
146	IM000764	GCACTAGGAAGGAAATTGACCCGTGTTG TTGGTTTGTGTTCTGGTTTTGTTGGTGGT GCTTTTGTGTTTTTGTGTTGTTTTT TTGTATCAGGATC	p000845	R	--
147	IM000765	GATCCTGCTTTCTCTTTTGACACAGAACA CTTCTCCTGATTGACTCTGGTCCAGACAT TTCTTTCAAAGGCAGAGGACTCTGGCTT AGCTGTGGATGACTTCTCAGATGAAGTT CATTGGTTGCGATTGGAACGTAATCAG AGCAGG	p000847	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
148	IM000766	GATCGCATTAGGGTTTTTTTATGGTTTC TCATCTTCTCTTCAAATTAGCATAGAAGC CTCTTCCTAAAGAATGGATACTTAATTCT TAACTTGAAAATATCTTTTCTCTGTGTGT TTCCTCTCCATTGACTGTTTCGCTCTATCT ATCTATCTATCTATCCATCTATCTACTGA AATTAATAAATAAGGGAACGCCTTCTTCTC TTCATTCTTGTTTGTGTTTGTGTTTGT TTGTTTTTGAGACAGGGTTTCTCTGTGTA GCCCTGGCTGTCCTGGAACCACTTTGT AGACCAGGCTGGTCTTGAACCTCAGAAAT CTGCCTGCCTCTGCCTCCCAAGTGCTGG GATTAAAGGCGTGCACCACCACCACTG GCTCTCTTCATTCTTTTAAAACGATTTT GAAACCTTTTTAGTGAGGTCAACATTGTG TACTCCAGTCCCACTCATCTTCCTGTCCC TTCCCTCTTAGGCCTGCCTGTCTGGTAC CTCACTCATGTTTGTGTATTCTCTGTGCT GAGCCTCTTCTGTGCTTTCCCAGCACAT GGCTGCTGGCTCCAGTTTCATTCCAGTC CCTTGTGATGTGAGCCTAGTTCAG	p000852	R	--
149	IM000767	CTCTCATGGCATGGGTCTCAAGGTCCTG CCATTTCTGCTCCATCTTTACCCAGCAC ATCCTGTAGACAGGACAAATTGTAGGCC GGAGGTTTTGTGGCTGGGTTAGAGACCC AGTTTCTCCACTGGAAGCCCTGCCCGGT TACAGGAGGTGACCAGTTTCTGGCTCCA TGTCCTCCATTGCTAGGAGTCTTAGCTG GGGTCATTCTCACAGATTCTGGGAGAT TACTCTATTTTATCTCCTTGTCAAAGTGT TCCATCAGATATTAATTATTCTCAAGATT CAATATTCTCAAATATTATTCTCAAGCTAT GGACCCCTCAAATTACAGATAGATTTTAT GAATGAAAAGTTGTGTGGTTTGAATATGT AGTTGAGGGTGACTTTGAACCTCTGGTTT TCCTGTGTCTACCTTCCAAGTGCTGGGG TTACAGGTATGAGCCATCACGCCAGTTT CTGTAGCACTGAGGCTCAAACACAGGGC TTCTGTCTGCTAGGCAAGCACTCCACCT ACCAAGCCAAATCCCCGGGCTTTACTGC ATCTTTGTGTGTATATGTATGGTATGTGC GTGTGTATGTAAGGATATATGTACCTGTG T	p000854	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
150	IM000768	GATCAACACCTGAAAAGTCGCGCCGCCT ATACACATCCCTAATTGAGAAGTATGTGG AAGATTCCATCCGTGAAATTCAATTATCA TGCAAGCCAAGTGGAAGCGCTTCCCTGG GGAAGGAACCCAGCAGCCGCATCAAAA CGACCCACCTGTCTATTTTCATGTCAAA AGAGTGAGAAGTCTGGGTGATGAAATAG AGAGCATACATCAGCTTAATGAAAATTC CAGGGGTCCTGCCTGTAATGGGAGTC CCAT	p000858	D	--
151	IM000769	GATCACCACCAGGGTGTTGAGAAAAAAA AAAAGCAAGTTAGTAGATGTTAG	p000860	D	--
152	IM000770	GATCTGACAAAACCTACCTGTTTTGAAC ACATGTGGGACAGCAGTCTGAGAGAATC TATGAATAAAATTCCTTTCTGAGTCTGGC ACATTGGTACAC	p000861	D	--
153	IM000771	GATCATTATACCCCAAATGGTACTGTATC TATATATACCTCAAACATGTCATGTAAA GAAAATACTCTGTTGAACTAATCACTTG TTT	p000863	D	--
154	IM000772	GATCACAGGACTGAATCACATTTATGCC AT	p000864	D	--
155	IM000773	GATCATTTATTTACTTGTTTTGGTGTTTCA TGTTTGTGGCTCCTTATGTAGTCTAGATA TTAACTTGAAGTCTGAAGTGGAACCTACCA AAGATTTTCTCCATCCTCATCT	p000865	D	--
156	IM000774	GATCAACCGCAGATGAGGTCTATGCAGG AAAAACGATGTCTGGAATTTTATTAATAAT TGCTCAGC	p000866	K	Myc
157	IM000775	GATCATCATGTCAAACCTGACACGTGAC GAGACAAATCTGTGTGCACAGAGGTGTG ACATCCTAAAAGTACTAACAATACCGCTG GGCAGGGACACACGCGGCAATTCCAGT CCTGGTATCCATGGCTCAAGCTCTGCAC GGAGAGCCCGGCACACGGCAGGAGGGA GAGCCACAGGCTAAGGAGAGCAATGCTA ACTAACATGGCACCCGTGTTAG	p000867	D	--
158	IM000776	GATCTGGCTTCCAAGGGCCTGTACTCAT GTCTACAATGCTCCTACACAGATATAT	p000868	D	--

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159	IM000777	GATCAGCCTTCCTCCAAAGCTACCTGCA TAGAAGAGACCTCTGCTCTCACCTACTC TCCTCTACAGTTTCAGCCCATATGGCTTCA CCTGCATCCCCCTACACACACACACACAG ACACACACACACACACACACAAACACGC ACACAGCACACACAACACACACAACACG CACACTCACAACACAAACACACACAACA CACACTCACAACACACTCACACACACAC ACAACACACACACACAACACACACTCAC AAACACACTAGTACACAAAGACTCCAAC ACACACATTCCCATGCACTACTCCCTCA GTATCCGCCGCATTTGTGTTACACTCAT CCACACTCTCACACATGTAGCACACACA CATCATTCTACACAGGCATGGACACAC ACATGCTCCTATACAGGCATGCCAGTA CTCTCACATGCATGTTTGCACGTTCCCAA ACAGGTTCCCAAGGGTTTGGCAAAGT ACATGCATCCTCACACGCTAATGCAAGC CGTCACACCCCATACCACAAGCATGCAC	p000870	R	--
160	IM000778	GATCAGATGTGGAATTAGAGAGAAGTT TTTAACGGCTCATGCACATTTCTGAAAAC TCTTTGCGAGGTATACTGGTAGATAAATG AACATTGGTCAGACTCCTCTAGTTTAAAC CACTCTCTTCCCCGCTATGGGGGGAGG CGAGAGGCATTTCTAAAGCTTATATGTAG TTGCAAAGTGTGTGGTGTGTGTGCAT GTATGTGCATGTGGTGTGTGTGTGTGTG CATGTGGTGTGTGTGCATGTATGTGCAT GTGGTATGTGTGTGAGTGGTGTGTGTGC ATGTGTGTGCATGTATGTGCACCGTGTT GTGTGTGTATGTGTGCATGTGGTGTGTG TGCATGTATGTGCATGTGGTGT	p000871	R	--
161	IM000779	CTAACATCTACTAAGCTTTTTTTTTTT TCTCAACACCCTGGTGGTGATC	p000872	D	--
162	IM000780	GATCATAAGGACTGTTAGCAGGCAAAGG CGCGTGCCCAATTAAAAGATGGCTTTCG TTCCAAGAGGAATACTCTGGCAAAGTCC CAAGCGCTTCGGAAGCCCCTCCCTTCGC TCTCCCACCCAGCTTTGATGCTCTGATT ATCCTAA	p000874	D	--
163	IM000781	GATCAGGCTGGCCTTAACTCAGGGAGA TTCATATGGCCCTGCCTTCAGGGTGCTG G	p000875	B	Mm.8363 5



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164	IM000782	CTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT GAGACAGGGTTTCTCTGTATAGCCCTGG CTGTCCTGGAATTCAGTGTAGGCCAGGA TGGCTCAGTCTGCTTTCTTATAGAACTCA GGACCACCAGCCCAGAGATAACACCACT CACAGTGGGCTGGTCCTCCCCACATTGA TC	p000876	R	--
165	IM000783	GATCACACACTTCACTGTGGCTTGTCAA CTGTGATTTGCTGATACAAGGGCTGTTTA CAAGTCAGCTATAGCTCCGCATTGCAGC TGCAAC	p000877	D	--
166	IM000784	GATCACTAATTGAGAAAATGCCCCACAG CTGGATTTCTGGAGGTACTTCCCCAAC TGAAGCTCCTTTCTCTGTGATAATTCCAT CCTGTGTCAAGTTGACAGAAAACAGCC AGTACACAAGTCGACACAAAAGTAGCCA GTACACAAGTCAACACACAACGCGCACA AGCTGAAGGCAAAGAGAACCAAGCATCT ACCAGGCCTCAGTTGCTATGTCCACTTC TGCAGCCACTCCAAAACACCTGTCAGAA ATTTCGGTTTGATAGAGAACTCACCGAGG GATTTCCCTAACACCAGGTCAACCAGGG CACCTCAAACCTGGAGGCACGACTGGCA CAATACAACCTAA	p000878	A	Cct5
167	IM000785	GATCACTTGATAAAGATGCTCTGAGCAG AGGCTCACAGGAACCCAGCCCTGTGTG CTCCCCAGGAGCGAGATTGAGCAGTCAA CAGTGCAAGTGTTCACGTGACCGTGCGCA GGCCATGAGCACTAC	p000879	B	AI615991
168	IM000786	CTCCTTTTCAGCAAGCTCCTCACATCACA GGCCTTCTCTTGGGATGGCAGCCGCCTT CTATCTGGAAAGTATGTGACAGCTCACA CAATCCTGTAAGTCTTCCATGTAATCACA TTCCACTGCCTCTCTGAACGTGCTCC ATGCCAGGGCCATGTGGAGGGAGCAGC AAGACTTGAGCTCAGCTAGTCTATGAAG ATGGTGGCAGAACAGGCTCTGCTGCCTT GATC	p000881	B	MMU767 54
169	IM000787	GATCAAGAGTTCAAAGTCATCTTCAGCTA CAAATGAAGTTGGAGACCAATCCAGACC CTCTCTCAGAAAAAAGGAAAAAGGAGA AAGCAAAAGGAAAGGAGGGGAGACCG AGAAAGAGAAGAGGGAAGGAAAGGGAA GTCAACAGAACTCAAGGTCAGCCTGGGA GGGTGAATGAGGCATTGTTGTCT	p000882	B	Mm.1388 09

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170	IM000788	GATCACCTCCACTTTATGGTGGACAGAG GATGGCAGTAGTAACTGCCCCAAGGAAA CAGAAACAACAACAACAACAACAAC ACCTCCAAAAAGACCAAAGCAGTAAGCT GTAGAACAAATGCAAAGAGCCAAAC	p000883	R	--
171	IM000789	GTTCCACCTATAAGGTTGCAGACCCCTT TAGCTCCTTGGGTACTTTCTCTAGCTCCT CCATTGGGGGCCCTGTGATC	p000884	R	--
172	IM000790	GATCACATGGACCGATTGCCGCGGGAC ATCGCACAGGAGCGTATGCACCACGATA TCGTGCGGCTTTTGGATGAGTACAACCT GGTGCGCAGCCCACAGCTGCATGGCAC TGCCCTGGGTGGCACACCCACTCTGTCT CCCACACTCTGCTCGCCCAATGGCTACC TGGGCAATCTCAAGTCTGCCACACAGGG CAAGAAGGCCCCGCAAGCCCAGCACCAA AGGGCTGGCTTGTGGTAGCAAGGAAGC TAAGGACCTCAAGGCACGGAGGAAGAA GTCTCAGGATGGCAAGGGCTGCCTGTTG GACAGCTCGAGCATGCTGTCGCCTGTG GACTCCCTCGAGTCACCCCATGGCTACT TGTCAGATGTGGNCTCGCCACCCCTTCT TCCCTCTTCATTCCAG	p000885	K	<i>Notch1</i>
173	IM000791	GATCATACGCAATGATTTCTTACCTTATG ATATAATTATGTTTAGAGGGAAACTTTT TTTTAAATTGAAGTTCATTTATTGTATGAA ATTATTTTCATAA	p000886	C	--
174	IM000792	GATCAGCATGGTCTACAGAGTAAGTTAC AGGACAGCCAGGGCTCCGTGGAGAGAC CCTTTGTCAGAAAAACAACAACAAAAA TTAGAAAGAGACCCTCTCTCTGATTTGAC CAATCACCCGTGTCAAATCTTGCCACAA CCGAATCACCACCAAATTGCCAGACAAG CGGCTATGCTGGGTTTCTGAGGTTGGAC TCCTCAGGTAGCCCGTGTCTAGGCAGAA TGATGCCAGCAGCTACACTTTTGAGAAC AAGGTCAGGTCAGGACTTGCCGCCAAAC CTAGGAATGCAGC	p000887	R	--
175	IM000793	GATCAGTCATGTCCTTTAGACGTTTACTT TCATCCCAACTTGGAACATTTCAGC	p000888	D	--

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176	IM000794	TTACAAAGGCAGAAATATCAGAAAGAGC CTGAAGTAGCAGCTGTTAACCTGTACCA GGAAGTGGCCGAAGTACACACGCGTTAA CTCAGCCCTAATTATTCTCGGGAGATAC AGTTGATTATCATACACATGTCAAAATGG AAAATAAATGGGTAACTAAAAATTGAGGA AAATAAGATTAACTTAAACAACCTAGT TCATTATGCCACGGTGATC	p000890	D	--
177	IM000795	GATCACAGTGGGACAGATTAAATGTTA	p000891	D	--
178	IM000796	AAACAAATACAAAGTGATAATTGTGTGAC ATCTGAACTTGTCAATGAGATAGGTAATT ATCTCTGGGCAATGGGTAAATGTGCTGG CCAGCAAACCTCACAGCCAGAGTTCAAT CTCCAGGAACTTAGGTGGGGAAGGAGAT AACTGACTTCCAAATGCTCACCCCCAAAT ATACAATTAATAAAAAATCTTCCTTTTAT GAGTAGCAACTGATC	p000892	D	--
179	IM000797	TACCCCTGGTCCTCCAACACTCCGATC	p000893	D	--
180	IM000798	GATCATGACATAGACTTGAGTCACTTCTC TGCAGTTTGTCAATAAAAGCCCCTAAGG GACAGTGTGGACTTTAGAGATAAC	p000894	D	--
181	IM000799	AATGCCAGCCATAGTGGCACACACTTTT AATCCCAACACTCAGGAGAAGTTAAGTTT CTCTTAGCTCAAGGCCAAGTAGCTTGGT CTACTCCGTGAATTCCAGCCCAACTACA TAGTAAACTAGCCTTAAAAAAAAAGGCA CAGGCAGAGGGAGATAACAAAAATGCCC AACTCCTAGCTACAGTAACTGTAGGAATT AAGATAGAATCTGTAGTTTGTATCATT ATCGTGATGATC	p000895	A	<i>li</i>
182	IM000800	GATCATGGCTTGATTGTAACATTATCAAA GCTTCCTTGGCACACTGCAGGGCTGTCT TCGGGAAACTGCGTATTGTGCTCTTCAG GTACAAAGCATAGAGCCCTTACATGACA AACGCTGGGGTTAACTTCTTCTAGTTCC CTCTGCCCCACTTGTGGCGCTTCCCACT CATGACTTCTTCAGTGTGTATTCACTT	p000896	D	--
183	IM000801	GATCATGCTGAACTCTTGAAAGTATTCTA GCAAAATGTGGCTTAAAAGAAAGAACAA ACATTAAGTATGCTTTGAAAAATTA CCTGTGGTAAAAATTCACAAGCATGAG AAGTTGTTTCTTTTGTGAACCTTCAGAC	p000897	D	--

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184	IM000802	GATCATATATCAATTTTATTTTAACTTTG TTTGTGTTGTTGTTGTTGTTGTTGTTGAG ACAGGGTTTCTCTGTGTAGCCCTGG	p000898	R	--
185	IM000803	ATTGTGTATCCAGAGTGTGACAAGGTAT ATATGGTTGTGTGATC	p000899	D	--
186	IM000804	GATCTTCTGTCTGGAAGAGTGCTTGCTG GTTCCGACTACTTTTTTTTTTTTTTTTTT TTTTNGCTTGGGTTTCANATTGGCTTCAG GTTCTGGGCCCTTCGTGGGTTGTGCTG CANAGCCCCANACAATGTCTTGGG	p000900	R	--
187	IM000805	CAGGAAACCAGGGGAAATGGGACACAG TGACATCTGAGTCCTTAGAAGAGGTCCC ACAAAGGTCTATATGACCTAGCAACGTC ACTTCTGAGTTATTTCTCAGACACAGTGG ATGTTTGTACAGCACACTGTAGGACAT CCCAGAACAGCACCATGGGAGACCATG GTTGGTGCAACAGAGAACATGCACACTG AGACAGTACAAGAGTTCCCAAGCAAGCA GACACAAACAATGGACTCAATACACATA CAGTGGCAGATC	p000902	C	--
188	IM000806	GATCTGCTCACCAAAAATCTTGTCTTAG GGAAGTTGAGTTTGAAGTGCCTGCTTAC TGGCAAAACACGCGGTGCCCAAATTTAAA	p000903	D	--
189	IM000807	ACAGTTCCCCCTGGAAATGGTCCCTGTA CCAGAGGAGCAGATC	p000904	D	--
190	IM000808	CTGGGGCCCAGACTCCAATCCCGAAATA TCATTAGCTGCTGCGCACTTCTCCGAGG AAGTTTACACCAGTACCCTAAGTTCAAGT CTCAGAAGCCTCCAAATCCTCGTTGCAC CCCTATATTTCACTTGGTCATCCGACTGT AACTCACTCACCGACAAGACAAAGAATA TCTTAGGCTCCGTGTAAGAAACGAGC CCGGTTCACCGCAGCTCCTTTTATAGTC TCCTTTGTGCGAGATC	p000905	B	Mm.2179 8
191	IM000809	GATCTGAAGATATTTTGACAACAGCTAAA AAAAAAAAAACCAAAAAAAAAACCCCTTATT ACTAACCAAGGGAAAATGCAAAAATAATT AAAAGTTCCTCAATTTTAAGTAAATATCC AAAAAGATTGGTTGTATAACAAAGTTGAA GAGTCAAACAGTATTTGAATAA	p000906	D	--

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192	IM000810	AGCTCATTGCCGTTAATTTTCCTCAGCCT AATGAGAATCTAAGCCTTGATTTGTATGT ACCATAGCATCTAGATC	p000907	C	--
193	IM000811	CCTTGAACCTAGTTCAGGGAATAGGCCA CCTGGGTGGGACTAGTGCTGTTGGGG ATGAAAAGACAGTTGGCTCAGGTGAACC CTGCTCGCACCTGGTCATCCTCTGAGA CTGCTTTGATTGCTGACCCCACTGCTCC AGCAAGAACTTGC GTTCTTGTCTCTCCA CTCAAGCCGGAAGAAATCTGAGGAGAG GGTGTGAATCCTGAGCCAGGATGTCAA AACAACGGAGTTGAGCCAGAAGGACGTC TAGTTGGGCAGAGTTAGCTCAGTCCCCT GACCCCACTCCGTGCAAGCTCGAGGG TGTTATATAGTGATACAGATC	p000909	D	--
194	IM000812	GATCTCTTCTTATCTCTACCTTTTGGGGC ACAATCTTATCTGGGGACACCACAGAGC CCAAGAATTGTCCTGTATCAGAAATTTGG ACCTTTTCTGTGGCTATCTGTAAACCCCA CTGACTTAAAGTTTTAAGTAGAAAAGGAT ATGCCTTTTGTAGCATGGTAAGGTCTTTA TGGCACAGGAGGATGTCATCCATGT	p000912	R	--
195	IM000813	CTTCCTTTCCTTTTTTGAACAGGGTTTC TCTGTGTAGCCCTGGCTGTCCTGGACCT CAATCTGTAGACCAGGCTGGCCTCGAAC TCAGAGATC	p000913	R	--
196	IM000814	GATCTGCTCCACTTTACACAGCTGACCA TGAGACCATGTNCACATAG	p000914	D	--
197	IM000815	ACATGACATATCACCCCTATTCAGAGTTC AGAGTCTTCAGAAAACCTGGGCGCCTGAA AAACCTGACCTTTTAAATTTTCGTCCATA GTTTCTTCTGTTGAATGAATATTCATTTAA AAGCTTCATAAATGCCAAGATC	p000915	D	--
198	IM000816	GATCTTCACAGCGCACCCAGGGATC	p000916	D	--
199	IM000817	CTTTTCTTGGTATTTAGGGAGTCAGGAA AAGAAAAACCATTGGGTTTTACATTAGC TTTCAGGTAGGGTTGTGGCTTTTGAGCA ACAATAACGTATGACCTTGTGGTCGGTT CTAGATC	p000917	D	--
200	IM000818	GATCTTCTTATATCTGGTTTCCTGGGCGC TTCCTGGTAT	p000919	D	--

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201	IM000819	GATCTCTGACAGGGTTTCAAAGAACTGT TACTGATGTTTAGATTGCCTCTGAAGACA TCACATATACTGTGCTACTCTGCCTTGTC AGAGTCCCGGGCCCTGGGCACCCAGAG CGGCAGCAGAGGAAGAGCGGGGTATCA CTTTCTATACTTCGGTAAAGTCATTGGGA TATGTGCCCT	p000920	C	--
202	IM000820	GATCTCCTCTATCATTTATCTTTCTTCCTT CCTTCCATCTGTTTGTTT	p000921	D	--
203	IM000821	GATCTGCTCACCAAAAATCTTGCCTAG GGAAGTTGAGTTTGAAGTGCCTGCTTAC TGGCAAACACGCGGTGCCCAAATTTAAG GAGTGCCAACGACTTCGCGGGCCAGCA AGGTGAAACCGAGCGCGCACGAGTGA GCAGTGCCAGGAGGCCTGGCCAAGAG GCCAGGGTCCCTGAGCATGACCGAGAG CTGGCGTGCTCTCTGTAACCCCAATCA GTTACCTAATCTCGGGTCGAAACCTGA GCCCTGCAGGAGGCGGGGCTGAGACTG CATCCAGCTCCTGGCCCGCTCCAGGG GCGACCC	p000922	D	--
204	IM000822	CCAGGCATCTCCATTCTTAATCCAGATC	p000923	D	--
205	IM000823	CATAGACTCTTTCAATTTAGAATAAAGTGT TCCACCTAACATCCTGTAGGAAGTGATG AAACTAAAAAGAAAAATAAACGCATTTTC TCTTTCTCTCGTTACTTTTTCCATTCACTA AACAAAATTGACTTTTTTTTTTCCATGAGA GTTCACTGCGGTCTGCCTCAGTAAGAG TCACACTGTTTCAGCCACACACGCTGTG ATATGTTATTTACTCATTCTCTTCTCAGG AACCCTCTCACATGTGAACCTGAATA CCAGCTCCCTCCCTCTTCAGATC	p000925	D	--
206	IM000824	ATAGGTTCTGTCTCAAAACAAAAA CCAAAACATGTCCACAGGGTCCAACAGA CACAGTCTCCGCCACTCACAATAATGG GTACACAAATACACACCTCAGCCTTACAT GGTTACAGAGAGAAGCAGGACCACAAG GTAGGCAGGCACCTAACACTTGCTTCTT GGAAGTTGGAGCACACACACACACAG AAACACACACACACTTTCTCACACTCACA CACACATTCTCTCTCTCTCACACACAC ACATGCACACATGGTCTTGTAAGCTC CTCCTGGGATGGGCACACACAGGGGTA AGAGGACTCCAGATC	p000926	D	--

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207	IM000825	GATCGAACACNCTNGGACTTGNTAAACG NTTCCACACNGACAGA	p000928	D	--
208	IM000826	GATCGTCTGGCCCGACCGCGCCTCAGT AGATTGCGGTCTGGTCTGAGCAGCCGG GCTGGTGCGGGTGTCCTCACTAGGATAA TGAATACAGCTCCACTACCTATACTACCC AAGACGACCCCTCACACGCTCTGCGAG GAAACCGGTCTTCGGAC	p000930	D	--
209	IM000827	GATCGACCGCAGATGAGGTCTATGCAGG AAAAACGATGTCTGGAATTTTATTAAT TGCTCAGC	p000933	K	<i>Myc</i>
210	IM000828	AGTAGACTGAGATTTGTGAGCGCTAAGA TAAAGATGAGCAAAGCTTTGGCAGCTCT TAGGTATCTGAGGGCCACCGTCTCTAC AAAGCAACGAGAGGCACGGCGGATTAG GATAGACTGGTTGCATCCAAACACTACC TTGCTGCCTCAAAGGCTTATTGGACACC ACAGAAAGACCTCTGCTGGAGGCAGAAG TCACAGGACTCCTCGTCACAGACGATC	p000934	D	--
211	IM000829	GATCGGCCTTCCTCCAAAGCTACCTGCA TAGAAGAGACCTCTGCTCTCACCTACTC TCCTCTACAGTTCAGCCCATATGGCTTCA CCTGCATCCCCTACACACACACACAG ACACACACACACACACAAACACACAC ACAACACACACAACACACACAACACACA CTCACAACACAAACACACACAACACACA CTCACAACACACTCACACACACACACAC AACACACACACACACAACACACACTCAC AAACACACTAGTACACAAAGACTCCAAC ACACACATTCCCATGCACTACTCCCTCA GTATCCGCCGCATTTGTGCTCACACTCA TCCACACTCTCACACTTGTAGCACACAC ACATCATTCTACACAGGCATGGACACA CATGCTCCTATACAGGCATGCCAGTAC TCTCACATGCATGTTTGCACGTTCCCAA CAGGTTCCCAAGGGTTTGGCAAAGTA CATGCATCCTCACACGCAAATGCAAGCC GTCACACCCCATACCACAAGCATGCAC	p000937	R	--

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212	IM000830	ACACCACATGCACATACATGCACACACA CCACATGCACACATACACACACAACACA TGCACATACATGCATACACATGCACACA CACCCTCACACACATACCACATGCACA TACATGCACACACACCACATGCACACAC ACACACACCACATGCACATACATGCACA CACACCACACACACTTTGCAACTACATAT AAGCTTTAGAAATGCCTCTCGCCTCCCC CCATAGCGGGAAGAGAGTGGTTTAAAC TAGAGGAGTCTGACCAATGTTCAATTTATC TACCAGTATACCTCGCAAAGAGTTTTTCAG AAATGTGCATGAGCTGTTAAAACTTCTC TCTAATTTCCACATCCGATC	p000938	B	Hs.17043 4
213	IM000831	GCTGGACCCCGGTGACAGACTGTGCAG ATGGATC	p000939	K	<i>Pim1</i>
214	IM000832	TTAGCAAGTCCGAGCGTGTTTCGATC	p000941	K	<i>Nmyc</i>
215	IM000833	ACTGCACACATTGCCGTTGTCGATC	p000943	K	<i>Notch1</i>
216	IM000834	CAAGTGTAGACATTGCAGGAAAAAATAT GGTGACAGTGAACAAAGCCCGTGAAGGT GACAAAAGCCAGTTAAAGTAGGACAAGG CAGAGCGAGGCCCATGACCGGGACCAG GCCCAAGAAAATAAACGAAGGCCACGAT C	p000944	B	AW32146 8
217	IM000835	GTCGGAGGAGCTGGCTGGACCGGTACA TGCCCTGGCCATCCAGGCGAAGACCCC CGCCCAGTGGAGAGAAAACCCACAGTTG GACATTAGTCCCCCTGCCTAGGTGGGA GCAAGAAAACCTCGAGGGACCTCTTAATA AATACCTGGATTGGGAGAACGATC	p000946	R	--
218	IM000836	GATCGCGGGGCTATCTATAGAGTCCCCG GGATGTCTGAGAAATCAGCCCTAGAAAT GACTAGAAAGAAAATCGAAGTATTCTTG GCTCCTGGAGACTTCCGCAGCGAGAAGT CACAGATTCAGGACACAGATTGACAGGA GCTGCGGGCGCTGGTAG	p000950	D	--
219	IM000837	GATCCCAGGATTTGGGAGGCAGAGGCA GTTGGCCCCA	p000953	R	--
220	IM000838	CAGGCTGGCCTCAAACCTGCAGAGATGC TCCTGTCTCTGAGTGTTAGATTTAATAAA GGGGTTCACGATC	p000954	K	<i>Lck</i>



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221	IM000839	GTTGCTGGGCCCTAAGCGCCACATTT ACAGCTCCGATGCTCATCAGCATGACTC TCCTGAGCACATTATCTGGTGGTGGCTG ACACTCTCTTCAGTACCCCCCCCCCTCC CAAAAAAGAAAAAGAAAAAGGACTG GTTGCTAAAAGAAGTAAAAGTCAAGTCAT CAAAAACAATGTAATATCCTGTGTGAAAG TCACGAAGCCTTGCGTTTGAGTCCCTC GATC	p000955	D	--
222	IM000840	GATCGGCCGGCTGTCCAGCGACCGGAG AAAGGAGAGCACTCGAATCGCAGAAGCT ATCAGGTGAGTCCGACCTCTCTCTGAAT GAACGCTTTGGGGAGCCTGCCAACGGT GACCAAATTTAGCCAGTTAAAGTACAG GCTGCCAGCTGTAAACGTACATCAAAC AATGTGCGATTTATTTTAGTGTGAA	p000956	D	--
223	IM000841	ATAGTAACACTTGGGAGGAGCCATTCCC AGTGAGGCTCGTATAGCATAGCCCTGTC CAATAGAGCCTCTGTTGCACTCTGTGTA CACTTAGCTCCTTGCTTAGGGATTTTTT TACATGGGTGACTACAGCACCCCAATTT CACATTGGACAGACTCCAGGACACCCCT CGGTGTCCTGTGACGCATACAACAGCCC CCCACGGGGCTGCACCGAAAACGCCAC AGTACTGAGGCTGCACCTCACTCACTCA CACACACCTCTATGGCTCAACGTCCTGG AGAAAAGGCTGCGACAGATTCCCACATC TGGGAATGCAGTAAAAAGCACTCACAC TGGGGGTGGGGTGGGGCTGGGGGGGC ACCCTGTCTTCCCGTCTTCCCATGACCC TCTTCCCTTCCAGGAGACCATAGCCAGA GCTGACAGGAGATTCACTCGCAGCTGCA CACGCTGCTGCCTTGCCGATC	p000957	D	--
224	IM000842	GATCGGGCAGGACACACATTGGGGAGG CCCATCAAGCCCGAGCCTGCCTTGTGAG CCCCCGATTGGCAGGGCAGAGAGGAA AGCTGCTGCGTGCTTTATAGACTTTGGG GAAGTCACAGGCTCCGCTTGCTTGGGG GAGGCAGGAAACCCCTCCACCTAGGC GTCTGCCAGAGCACCCGCAGGCTTCCTC TTGTCTCTGTCCCCCTCCCAGCACCTC TCCCCCTGAACAGCTTCCCTCTCCTGGC CCTGCTGTCCCTTTAAAGGAATTGAATC AGAGTTGAGAATGATGGTGACTCAGGGT GGAAGGGGTGGTCACTTG	p000959	D	--

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225	IM000843	CCAGGGCTACACAGAGAAACCCTGTCTC GAACAAACAAACAAACAAACAAACA AACAAAGTTAAAAATAAAATTGATATACG ATC	p000960	R	--
226	IM000844	GATCCAGGACATGGCAGAATATGGTCAT CTTCTTTGCTTGCATGTCACACGAATGG CCTCTGGCTCCACCCCTGATTGCTTGCT CCCCTTGGAAGCCTCTTGAGCCTAGCTA ACTTTTCCTGTTACCTTTGTATTATGTG CTCCCACCATGGCCCACCAGGCTCTGCT TGCAGCACTGCAGCCTGCAGCTCCAGC GGCCTTTACATGGCTCCTGTAAACAAGT CCCAGAGGCCTCAGTGTCAATTTTCTCAG CAACCGCCTCACTTCTTGGTGCCGCCTT CCTTTATTACTTTTCAATTTCTGTGACCG AAATACCCCCAAAGAAGCTACTCAAGGA AAGCAGTATGTGTGGGCTCACCATTAGA GGTCAGTCCCCTGCAGCAGTGGAAGCAT GTGCTGGTGACGC	p000976	D	--
227	IM000845	GATCGCTACTTTTTAGAGACGCCTTCAT TAAGGGGAGAATGGAAAGATGCTGGTTG ACTTGAAAGATTTCTCTCTGATTTGTTTTA CAGGAAGTGCATTCTGTACACATGAGAG ACTCCGGGTGGAGAGGCATTGTGGCGG TTGAGATGCACCTGGGAGTGCCAACTGC CCCCGCTTCTACCACAGCTCTGCATAGC AGGCTGGAGCAAGCAGCCAGCCAACCA TTGTGCCCTAGCCTCATCTCCTCCAGAA GAGGTTATCTGGGCTCTGTGTAACCTCT GCTCTTTGGCTATGGTATTCCTTCTTGGT GCTTTCTGTGGTCAACCTCCAGGTACAC TTAGGGCCTATCCTAGACAGACTGGGAA GAAAGAATGACATTCCCATTGACCTCTGT TTTTATTTCCTGGAAATCCAGACCTTGTT CCAGTTAGTGGAGCATGGGGTTAGACCA ACCACACTGCTAAGAGTTTTGGCCTGTA GACATATCTGG	p000983	C	--

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228	IM000846	TAGCAAGGTAAGTACTTGTCTCAATTTCC AGGTAGTATAGAAGAAACATATGTTAC AGCTTTAACACCAGAACAAATCACACAGT GTTGTATTTTAGCTAAAATATGACTCTGT GGTTTTCAAATGGCATAGTTGTGGACAA CTTAATTAAGCACGCTCTTATAAGACGTG ATAGAGTATGTGCCATCCAGATACTAAG AACTGTGTCCAAAGAGCTTGGGACACAC ACTAAGGGGCCTGCCTCTTTCATAACGG GGATGAAAATGACTGAGGCTTCACATTT GCACAGTACGATC	p000988	D	--
229	IM000847	AAGCCATCTGGGTCTCAAGTTGCTAAAA CTTAATAACTCCCTCCCTGTGTTTGTCTT TTATCTAATGGTAAAATATGACCTAATGA AATAGGTTCTAAGGCTTTCATATAAGGC ATGATGTTGAAGGATGGAGGACAGAGTG GGATGGAAAATCAGAGCCTGCACAGAAA ACCACAAGCAGCTAACAAAAGTCCACAA CCAAAGCCTGTGCCTGAAATGTCACCTA CAATGCAGTGGACTATTCATATGCCAGC CTGGTCCTCATGCGATC	p000991	D	--
230	IM000848	ACCAAGAACAGAGCCCCAACTAATAGG ATGGTTTGTTGCACGTGTACATGTGTATG CATGCGTGCATATACGTGTGTGTGTGTG TCTGTGTGTGTACACCCACACGTGTGCA TGTGTGTTGTGTGTTTTTAAAGCAAACCT CAGTGTGTCATACATACTCTCCTATACTT CCCCTCCCTTGTTCCATATGAGGGTGCC TTCTTATCTCACAGGGTTGTTTTGTTTTT TTCTATAACAGAATGCCGCTGATGCTCTT TTTTCTATATGAACCCTACATTTAATACTT ATCCATAAGCAAAGGAACAGTATCTTATC TTGCGGATC	p000992	R	--

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231	IM000849	CTGGGGGCTCTGCTACGCGTCAAACGC CTGGAGAACCCCTCGCCCCAGGCGCCG GCACGCCGCCTCCTGCCTCCCTGAGCG CTGCTGCATCCTGCACGCCCTGGAACCC AGGAGCGCCCCAGCGACCCTGACTCCC TGCCAGCACGTCCAAGGCTGCTTACCCC AGCAACCTCCCATCCCCTGAGCCCTCAG TAAATGCCATCTGTAGCAGCTGTTTGTCT GAGCGCCCTGTACTAGGGGGCCGGTGG GCTGGGTGACAATGATAATGGAATAGTG GCTGTCCTACTGAGGACAGCACAGTACT GTTTGGGACCTGTACTGGTAAGGAATAC ATGCCTGCTTCCTCTGGACTTTGCGGGT CTCACCGGGTGCCTGGGCTACCCTTCTA GGCTTCACTGAGGCGGGTTCCTGGGA GGCTCTGAGGTTACTTTCAGCGTCTGCC AGGGGTCCACAGCACTTAGCCAAGGGG CTATGGATTCACTCGTGGTCTGCCAGGA CCAGGCTTGTTGTGAGGGCCCCAGGTG GATC	p000993	A	Saas
232	IM000850	GTGTTTCTTTTCTTTCTTTTCTTTTCT TTTCTTTTCTTTTCTTTTTTTTAAATCTAA GTAAGGTGCAACAATGTAATTCGAAGGG GCAGTGTCTTCCCTCCTGTAGTCTCTG CTTAATTCCTGAAGTTTGCCAAACCAGGA GTTAGGAAAAGTTGAAACCTGCAGAGA GAGCGTTTGAGAGGTTTGAGATGTTATA CGAGAGGGTTTGGCAATGTGTGGAGTAC AGGTAAGTTGCGGTTATTGTTTCTTGCC CCTCTATCTTCATCCTTTGTGCTTGCTAT TTACCTTGCTGTCGGATC	p000994	R	--
233	IM000851	GATCCTTGAGTCTGTACTTAGCCTGAGA GCGCTATAACACTATATACAAAGTACCGA CTAGAACTCCACACACATTTGTTGACTG ACTTAATGTGTAGCCCTGCAATGGTTGA CAGTTGGGGGTCAGGGGGCTCTTGCAC TGAGGGTAGTGTATAGCCTAAAGAGATA ATCAAGATGATAAGTACATCCCACTAG GACAGGAGCTTTAACAAGAGCTTTTAGT GAAGGGAACCTTCTGGGAGCCTCAAGGA AGGCATAT	p000995	D	--

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234	IM000852	AGCAACACCTCATGTGGGAATTCATACA TTGTAGGTAATCAGTCTACTAGCTGAACT ATATCTCCAACCCAGGAGGTCAGGTTTG TTTGTTTGTTTAACAATCTAGTTTTGAAAC AGTCATATCCTAGGCTGGCCTCAAGTTA TGTAAGTCAAAGATGGCCTTAAAGATGA CTCTTGGTTATTTTCCAAGTGCTGGGATT ATAGATATGCACACCACCACACCTCATTT GTCTCGGGGCTGGACTCAAATCCAGAGC TTCATGCATGTGAGGCAAGCACTGTACC AACTCGACTTTTGCATACTCCATTGAAAG TCATTTTATAACAGGATC	p000996	D	--
235	IM000853	CTACTTATCTATCATCTATATGTCTATCAT CTATCTATCTATCTATCTATCTATCTATCT ATCTATCTATCATCTATCATCTATCATCTA TCATCAATCATCTATCTAGCATCTATCTT CCAGAGCTCATGTTGTGGCTTGGGCTTC TCATTTCAACATCATCGAAGGTAGTTGCA TTTTTCTATTGGCTTCTTAGAAGCAGGA GGCACATGAAACAACTTGCTAACCCCTTT CCTGGTCTTTTGTGTTGTTGGTGGTGG TGGTGGTGATGGTGGTGCTGGTGGTGG TGGTTGATGTGCACAGGAGACCTGTCCG GTATGGAGATATGGAGAGCGTCTACGTC CTCATGGGATC	p000997	R	--
236	IM000854	GTGGGACGCGGAGGGTGGAGATGAATT GAGAAGCAGTTGTCGATTTCTCCTTCTT CCAAACATCAAAGGCAGCGGTGGATGAC AAACTGAAGGACAGAGGGTTTGATGATG CAAGAGGAGCCAGCAGCAACCAAGGCC AGCCTCTTGCGGGTGTGGGCAGGGCCT TCTTTACAATGAGTTCACACACACACACA CACACACAGAGAGAGAGAGAGAGAGAGAG AGAGAGAGAGAGAGAGAGAGAGAGAGAGA GAGACTGCTCTTTCAGAACAGCCCTAGG AGGTTAGCTTCAGACTAAGACAGGAGAC AGAGAGTCCTTGATTTTGCCAAGGTTGC ACAGCTGGGGAGAAACCCAGCTATGGCT TCACCTTGGCCCTTGTTAGGACTCCTTC CTAGTCCGGTTGCAGTCTCCTGGATC	p000998	R	--

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237	IM000855	GTATTAGAGGCCAGGCCATTGAGAAGAT GTGGCAAGATTGTCATGTGGAAAATATTT GAAACCATTCTAACCTAGTCATTCCATCA TCAATAATAATAATAATAATAACTACTA AAATGAAAAAACCTAGATATTTTGAGACT GTACTGCTGTATTTTAAGAAATACACGGA AATTTAGCACTGAAATTTAGTGCTAGTTT TAAGAATACTTTGTACCGTTACTTGGACC CACAATTGCTTAGAGCAAGGGATC	p000999	C	--
238	IM000856	GATCCTGAGACAGTACAGGAACTAAGAA GCCCTGGGCAATTTGCAGTGTGCACACC CAGCCTGAATTTGCCTGGTTCTCACCAG CCTACCAATAGAGCATTGTAGTGGCAGG GATGTCTGCTGGTGTCTCGCAGACAAC TTTGAGGTCTGCTTCTCCAGAAGTGTG CAGCTGGCAATTAGCAGCCTGGTCTTTT CCTGTCCCAAGACCAGTGCTTCCACCA ACCTGGTCTCTTCCACAGCCCAGCCCT TTCTCTTCTCTTTGACACCCACTTCCTC TAAATGGTGGTCACATGCTTTGTCTCTTG AAAAAAGTTGTATGAGTCAGGGTATTTT CAACGCCGGGACAGAAAAATTGACTCAA CCTGGCTTTTTCAATTAACCACTAATGGG TTTCACTTACAGTCCTGACAAATACCAGG CACAATTCATCCAGGACAATAGTGAAGA ATTTTCATCTCTTCCCCCAAGCCAGTCA GTCTGGTTTTAATATGCACGGTGGATAG CCCATAGCATGCAATGAACTGTGAGCAC CCCTCTGGGAGTCAGCAGAGACACACAC ACAGGCACCCATACCACACACTGTGCTT TGATCA	p001000	D	--

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239	IM000857	GATCAAAACAATATTCAAATAATGACATC AGTCAAAGTATGATTTGATGGCCATCACT CATGTCAATAGGCAACACATAAGCCTGA GAGTAAGTTAAGGAGAAATTCAGCAATA AACAAATTGACATACTATGTCCACTATGA GTAAACCTGCCTCTCTTAAACGTTTTA CTGTACTCCATGGCTCTCCCCAATGTG CGTTCGTGAGAGTCCCCACCCCTGTGAC TCCATCTGTGTGTGGGTTCAAGGAGAGAC TCCTGTGTGTATTCAAAGAGCCCCCA TGTGTGTACACACAAGAGACCCAGTGTG TGTACATGAGAGGCCCCACCCCATGTGT GTTTCATGAGAGACCCAACCCCTGTGCGT GTACATGACTCTCCCCATGTGTGTTTATA AGAGACTTGTGTGTATGGGAGACTCCAC CCTGTGTGTGTACATGAGAGACTCCTGC CTCTCTGTGTATATGGAATACCTTCAGA GTATCAAATATTTTCACCCACTGAGCCAT CTTAGAACTTCTCTCCCTT	p001001	C	--
240	IM000858	ATACATATGTACACACACACTCACAAACA CACATATATACACATACATACTCAC ACATATATATACACACTAGTACACACATA CGCAAATACACACATGCATATACACGTA CTCACACATACATACCCATACTCACACAA ACACATATATACACACATACTCACATATA CATTACATACACACACATATATACAT ACACACACTTGCATACACACAGCACACA CTCACACACAGAGACACACAGACACACA GACACACACACAGAGGAACCCAAAGGAT TGGAAGAATAATTTCTGTGCTCAGTGG GAAAGTTTACCAGAAAGACAAGTGGTCA TGTGGGATGATC	p001005	C	--
241	IM000859	GATCAGGGACCCTGTACCCTCCCCCGTG CAGCCTGTGATTC	p001006	C	--
242	IM000860	GGACTGTAACCAACTCGGAGAGGAAAG GGCTTATTTTATTTTAGTCTTTACAGTCC ATCATTGACGGAGGTTAAAGCAGGACGC TGCTTACTGACTTAGCTCCCCGTTGCTTT ATCAGCTACTTTCTTAATAACAACGCCACC CCCGCGGCCGCCACCTCCCTAGGCAAG ACCCACAGGTCAATCCAACAGAGAGGAT TCCTCAAGTGACACTCCTATGTCAACGC TATCAATGGCAAAGGTATATTGAGCTAAG AATTGATC	p001007	D	--

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243	IM000861	GATCTCAGGCTGCCCGTGGGCGGGGCT GACGGAGGGAAGCAGACTAGGCCTCTA CCATATCCGTGGGAGGGACTTCCAAGGA CCGAGACTGAAGAAACAGCGCGAAACA GGAGACACTGGGAGGAGAGGCGGAGAC CGACACTTAGTAG	p001009	B	Mm.7675 3
244	IM000862	AGAGAAAAGACTATCTTGACCTTTGGATA TGCGGGTGCAAAAATGAGAAGACCACAG TGCAGCTGTGTGCCCTGCACGGGGCAG CGAGAGGAGAAAAGAAGCATTTTACATGA AGCACAGAACACGCCTGACAGTTCTCAA CAGCAGCACGTCAGACCACCGCAGCAC TGCTCGTTTTTCTCAGCAGACCCCCAGG AAGCACCACCCAGGATGGACATGTAGG GGTGCATCCGAGAGAATCAAAATCACAC AGGGGCCATCCTTTTGGTTCGGCATGAA TGATGGGGGCCGCTGCACTGGCCTCC ACCTTCTATGGTTGTTCTTCTTGTATCA ATGTTTCAAAAAAATCCTTGGGCTCACA ACTGCCTAATGACATCTTCAGGAGTCAA GTCAAGAAAGAGAAAAGTAGCCGACCTG GCACGTGGTAGATAAGACTCAAGGGTGC AATAAGCAGATGAACTGGCTTAGTTGGG CTTTCTATTGCTGTGATAAACACCATGA CCAAAGCAACTGGGGCGGGGGCGGG GGGTGTCATCTTACACTTCCATATCACAG TCTATCACTGAGGAAGTCAGGGCAGGAT TCAGGCAGGAACC	p001011	R	--
245	IM000863	GATCGGCCAACACAGGATAGATACCACA CAGGATAGGAGGTACAGTGTCTGGAAGA TTATTATCGAGCCCCTGAACGTAGTAGA AGCTGGCTGTCGTTCCAGTGCAAGCTGA GCAGATGGTCC	p001013	D	--
246	IM000864	GATCCACATGAAAGCCAAGCTGCACATT TGCTTCATATGTATGGAGAGGCCTAGGT CTAGCCCATGTATGTTCTTTGGTTGGTG GTTCAGACTCTAAGAGTCCCAAGGTCC AGGTTAGTTGACTTTGTTGGTCTTCCTGT GAAGTTCCTATTCCCTTTGGTGCCGTCA ATCCTTCCTCCTATTCTTCAATAAGAGCC CGCAAGCTCCATCCACTGTTTGCTTGTG GGTATCTGTAA	p001015	R	--



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247	IM000865	CCCTCAGCTACATAGTCAATTCCCATCTA GCCTGGGTATGCGAGATGGCAGTAAAGA CACTAGCTGCAAAGCCTTACTGCCTGAG TTTGATC	p001018	D	--
248	IM000866	GATCCAGTCACAGGAGAGCAACTGGGG GAGGGAGCAGGACAGAAGCACACCATA GCCCTTTCAGGGGGCCGGGGGCGAGG GGTGGACAAGAGAAGACAGATAATGACT CACAGGATGAAGAAGCCTCCCACAGCCC CTCCCTGAACTGGCCATCTGTTCTGGGG CCCCAGAGCAGGCGAGTACCGTGAAGC TTGGGGACTAGCAGCCGGACCACTGAA CAAGGTCAACCAGCCAGTTGTCCCACGA GGGGAGAAGCTACCATTGAACTGTCACT TTGGAAAGTAGCCAGAGCCCATCCCTGG TCACCACCCAAC	p001019	D	--
249	IM000867	GATCCCTAGAGCTGCTGGTCAGCTGGCC TGGCTGAAACTACTTCTGTGCAGTGAGA GACCCTGCCTCAAAACACAGATAATGGA GACAGATAAATGACATCGTCCGCTGTGT CTGCGTGTGTATATGTAAACACAACACAC AGTATACACACATACACACCACACTCATA CCGTCACACATGCACTCTCAGTGATGT GCAACACAACACAGTGTACACACATACA TACACACCACACACATACATACCACC ACACACGCGCACACACACACATAA	p001020	R	--
250	IM000868	GATCCTTGTGCATCACTGAGCCATCTCC CCAGCCTACAGTGTAAGTATTCTATACAT ATTAATTTAATCCTGCCGGGTGGTGGTG GCGCACGCCCTTAATCCCAGCACTCAGG AGGCAGAGGAAGGTAAATTTCTGAGTTT GAGGCCAGCCTGGTCTACAGAGTGAGTT CCAGGACAGCCAGAGCTACACAGAGAAA CCCTGTCTCAAAAAACCAAAAAACAAAA CAAAACAAAACAAAACAAAATCCTATGG AGTATTCTAAAAGTAAAACCGTATCATT GCACTGCCAAATAACAGAAAAGGAAGACC AAAGCAA	p001021	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
251	IM000869	GATCCTCTGAAAATGGAGTTACAGATGG TTGTGAGCTGCCATGTGAGTGCTGGGAA CTGAACTCGGGACCTTTGGAAGAGCTGC TGGTGCTCTTAACAGCTGAGGTGTCTCT CCAGCCCCTTTGGGTGTGTTTTGTTTTGT TTGTTTTGTTTTGCTTTTTCAAGACAGGG TTTCTCTGTGTAGCCCTGGCTGTCCTGG AACTCACTCTGTTAGACCAGGCTGGCCT CGAACTCAGAAATCTGCTTCCCAAGTGC TGGGATTAAAGGCGTGCGCAACCACTGC C	p001022	R	--
252	IM000870	GATCCAATATATTCATATGGAGATACATG TATATACATAA	p001023	D	--
253	IM000871	GATCCAGGTCCTTTCCCCCTTATGGTCC TATACACCCCTGGGTACTTAGAGGCTTT CAGCTCTGACTGGTGGTGTGGGGAGAA GTGAGGGGTTACACATGTGACACAGGTC CTAAAAGCTGTCGCCATTGGCACATGAC CATCCTAAGTCTGTGGCAGAAGGCTGCT CAGAGCCTCTGTCCAGGAACAACCCAAC ACATTGCAGAAATAACTGTGCATCTGGG CAATGGGGCAACTACTACCTGTCCATCC AGATAGCTCTTCTAGAGGCATTGAAATA ACACGTAAAGTGGGGTGGTGATGAACAC ATATAATCTCAGCCCCTGGGAACCGGAG ACAGGGGAGTCACAAG	p001024	D	--
254	IM000872	GTCACAGTACTTGCTCACTTGCCTCTCTC ATGGTTTACTCGCCCCCTCTCTCGTAC CCCCCTTCTCTCTACAATCCTCCTCGTCT ACTTTCATGCCGTATATGTCAAACACCGT CATATATAACAATGTATGCATGCAGCATT TCTTTTTCTTTCCCATCAGCCTCCCTTGC TCCCCATCCTCCCGCCCTTCTCCTTCC TCCCAGGATC	p001026	D	--
255	IM000873	AGTTATGCTTGCAGACAGGAATGTAGCA TGGCTATCCTCTGAGAGGTTCCACCCAG CAGCTGACTCAGACAGATACAGATACCC ACAAGCAAACAGTGGATGGAGCTTGCGG GCTCTTATTGAAGAATAGGAGGAAGGAT TGACGGCACCAAAGGGAATAGGAACTTC ACAGGAAGACCAACAAAGTCAACTAACC TGGACCCTTGGGACTCTTAGAGTCTGAA CCACCAACCAAAGAACATACATGGGCTA GACCTAGGCCTCTCCATACATATGAAGC AAATGTGCAGCTTGGTTTTTCATGTGGATC	p001027	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
256	IM000874	GATCGTGGTCTCTTCTCTTTTTCCCTCT ACTTCTTCTTCTTCTTCTTCTTCTTCT TCTTCTTCTACTGTCTTCTTCTTCTTCT TTCTTCTTCTTCTTCTTCTTCTTCTCTC TCTCTCTGTCTTCTCTGTCTGTCTGTCT CTGNCTCTCTGTCTCTCTCTATCTCTGTC TTTCTCTGTCTCTCTGTCTCTGTCTCTCT TTCTCTGNGNCTCTCCCTGTCTGTCTGT CTCTCTCTTCTCTCTCTGTCTCTCTCTC TCTGNCTCTCTNTCTCTGNCTCTCTCTGN CNCTCTGNCTCTGTCTCTGTCTNTGTNTN TCTCTCGCTCTCTNACACACACACAGAT GTACATGCAC	p001028	R	--
257	IM000875	GATCGGCGGTATCATATTTTATGTGTTTT ATTTCTGTGTCTAGAAAGTTTAAAAGGCCT CAGATTGGAAGTCTGGTTTGCATGGAAT GCATATGAGCTTTTTCATCTTATTGCCCA ACAGATTTAGTCTAAGAACCACCTCTATT ATATAGGGTATGATAAGTAATATAGGTAA GGGAATGCATCCCATTTGATAAGTGAAA GTTGAACACACATAGAGTTGGCTCACCC CGGGGTCTAGGCTCTAATCCCCTGGGG ATACCCAGGCCAACTAAACGCTATAGCA ACAGGCATTGGGGCATGAAGATACTTTT TGTTGTTTGTCTTGAATTTATATAGGGGC TTATATCTCATTACAATTAATCATGAGTTG CAGTCAATAAATCTTCATTGCTCAACATA TTTGTACCCTCAAATATTTTTTCTTTTTT TGTGTGATAT	p001029	C	--
258	IM000876	CTTGTAACACGATTATTTTAAAGATATA AATGGCTCTTACTCTGTTTAAAAATTGT TTCTTTACCAGTTCTTCGTGTACATTGGT CTCCATTTACATGAAATAAAATATTTTGT TTAATGTTAGATTTTCAATACCAGCTGAG TGTTTCGATGTGTGCCTTTTGGACATATAT TTGTTGTAAAGTGGTCATTTGGGATC	p001031	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
259	IM000877	GATCAGATTCAACTCCCGCATTCTAGC CCCAGCATCGTGGAAGGGCTACTGTGTC TTTTCAAGCACTATGGTGGATACACATAA TGCCAGCTTCCCTCATTACTGGTGATGT GAGCTGTTTGCCTAAGGTCCTTTCTGCC AGGCTTCTCTGCTGCCAAGGCTCTGAAT TTCCCTTTGTAGCTAATGCGTAGCCCTAT TGGCAGACTCTTCCCGTGGCTGACTTCT GCCTCCCGTCACACAGCAGTACCTTGTT TGTTCTCACCTTGATGTTTCTTATATGCA TTGATGATGGTGAACAGCCCAGCAAGTG CGCCTGTTTCTTCCCTTCCTCCCACTTTT GTTCTCAGTTGTACATGGCAAGGAAAAC CAATTCCTTCTTTCATATTTCTCCAGAA AAAAAATCCTCTTTATAAGAGTTCACATC CTTGAGCACACATGATAGGAGCTGGTAG CCAG	p001032	D	--
260	IM000878	GATCATGATATTGTACTGCTGAAGACAAA CATATTTAAGATATAAGACTTGGAGAAAT CAAGTTGGTATTGACATTGGAGATTAATC TCTTTTGGCTAGCTTTTGTAGAGCTAGAA GTTGGTATGTAAGCTATAAGGAAGAGAA GTATTCATAAGACTTACCCAGTTGTCTCT CCTGTAAGCTAAGACCAGCCTAAGAAGC TAAAATTATCTTTAATGTAGAACCACAGA GAAAGAAATTGTGGTATGAATTTTGCTTG TTCGTGGACATTAACCATTAACCTCAATGA TAATCAAATGACAATACATAGAGACAAAG ATATGCATACTAGTAAATAGTGATAA	p001033	D	--
261	IM000879	GATCGTGCTAGAGAATGGTACACTTGGG TTATATTAAGAAATCTTGGTTGAGTGGTG GTGGCACCCCTCCTTTAATTCCAGCACTC AGGAGTCAAAGGCAGGCAGACATTTGAG TTTAAGGCCTGCCTGGTCTACAAAGTGA GTTCCAGGAAAGACAGGGCTATAAAGAG AAATCTTGTCTTGAAAAAACAAAAAAC AAAAAACGAAACAGTAACTGAAACCGAA AAAAAAAAGAAAGAAAGAGAGAAAGAAA GAAATCTTACAATGTGGGAGCTGGAGA GCTGGCTCAGTGGTTAAGAGCATTGGCT GCTCTTCCAGAAGACCCAGGTTCAATTT CTAGCACCCACATGGTGGGTCACACCTG CCTGTGGCTTCAGTTCTAGAGTTTCTGA CACTCACACACAAACATACATTCAAGT	p001034	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
262	IM000880	GATCTTGTATTTCTTCTTGGCTTGTCTCC ATAGGAACAGGCAGCACAGCAGAGGTCT GGGAGATGGCTCCGAGGGTAAGGGACC AAGCAAGGTCACCTGCGCTCACTCCCTG GAACCCACACAGTGGACAAGAGAGAAAG ACTCTATGGCCTCCACGTGCGTGCGTGC GTGCTGTGGTGTGCACGTGCCCTCCC CCAAATAAAGAAAACTTAACGAAAAAAA TTAAAAGTAAAAAACAGCACTGCAGTAG CTCCAGGAATCAACTGGTCAATCAGTGT ATCACATTTGACTATCCGATGATGGTTTT ATTTTACATGTATGCACGTGTTTGCATGT ATGTGGGTGCACATGTACAAACACATGT GCCAAGGCCAAAGGACAACTTTGGGTGT CCTTTCTCAGGAGTCATCGACCTTATTTT CTGAGACAGGGCCTCTCACTGGAATCTG ACTGGCCAGCAGCCTCCAAGGATGCTC CCCAACCTCAGAAGGATGCGCCTGTCTC TGCCTCCCAGCCCCGGGGTTACACTG GTGGACCACTGGGCTCTTTTACCTGGG TG	p001035	B	Mm.1388 34
263	IM000881	GATCTCTTCTTAAAATTACATTACAGTAG AAAATGTTTATGAGGCCGTTTTATCTCT AATATTATTTATTACCACTCTCCTACCCC CAGAGTCTTACAGGCATCAGGGAGTGGA CAAAGGCCGGCGGTACTGAATGGTGAT GTTATTTTTGAAATAATGAAAAG	p001036	D	--
264	IM000882	TACCTGTTGCTCCAACATGGTCAGAAAT CAGTTTGTTCATTTTAAGATACAATGA GAGTAACACCCTAAAGACTTCACATTTTA TGCATATTTGCTACTCTGTGAGCACATGA ACGCTTCTCCTTGGGCACGATC	p001066	D	--
265	IM000883	GATCGCAGATACTGCAGGTATGTAGTAA TGAAGTCTGTAAACATACAGAAATGGAGA AGGCCAGAGAGGAAAGTGCAGGCATTG GGTAGTCAGTAGGTAAAATAT	p001067	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
266	IM000884	GATCGCAGCTCTTCCTTGGTGCTTTTCC CCTCAGTTCAAGTGCTGTGGCGGGGAG GACTACAGAGACTGGAGCAAAAACCACT ACCATGACTGCAGCGCCCCCGGGCCCC TGGCCTGCGGGGTGCCCTACACCTGCT GCATCAGGAACACGGTAACTGCATGGGT GCTGGATGTGAGGGTCACCCAGTTTGCC AAACACTGCCCTCACTCTGCCCAAGTGG AGCAGGCAGTGGGAGTGGGTGGGACGT GGTGGCCGGGGCTGAGCTTGCCCTAGA CCAGGGGCCCTAGCAATGGGAGATGAG TGGGCAGCTTCCTCTGGGAGTGTGTCAG TGAGCGTGTGCGTGTGTGGCCTGGCC CAGGCGCTTTGGTTGTAGTTACTTGGTT CTTACAACAGCTTTGGAGGGTCTCAATT GGGGTAGTGTTGCTTTAGCCACTTAGGG GGAATTGCCCAAGGTTGGCAGGGCTCTT CCCAGCAACAGAGAGCCAGAGTGCCCG GCAGGTGCAGCAGGCTCTACCCAGTCA CTGGAGGCAGAGTACAGTGCAGGTGCT GTGAGCACTGGCAGCAGAGCCCTGGGC AGCGGCATGCGGTAATGTAAATG	p001069	B	Mm.2811 2
267	IM000885	CCATGTCAGGTGATTAACCTGTGAGTCT AACTTCAGGAATGCAATGCCTCTGGCA TCTACAGGCATAAACATACTTGTGGCTTA CACTCAAACCTGACACACCAACACATATGT GCACGCGCACACACACACACACCAAATT AAAAATAAAATAACCCTTTTTAAAAAAAT ATAGAACCTATAGATAATTGCTTTACTGC ACTCACAAACATTTTAGGATC	p001070	D	--
268	IM000886	GGGGCACATAGTGAGTTCTAGGATAGCC AGGGTTATAGAAGCTATAGTGTGAGACC CTATCTCAAAAAACAAAACAAAACAAAA AAACAAAAAAACCTAAGCCCGTGTGGT GGTGTGTCTCAGTCTGAGCGCTTGGAAG ACAGAGGGAGGTGCATCTCTGAGCTTGA GGCTAGCCTGGTCTACATAGAGAGCTCC AAACCAGTCAAAGTAACAAAATGAACTG TCTCAACAATGACAACAACAAACAAACAA GCACTAGAATAAAAAAGAGCCAGCATGG TGTCATGTGCCCCTCATCCTACCACTTG GAAGGAGAGAAGCCAGTGCAGGAAAATT AGGGATC	p001072	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
269	IM000887	GATCCCAGGCTTCCTGTAGGCTAGGCAA GCCCTCTCCCCACCCTGTCCTGGTAGAA TTCATCCCGAATGTCAGCATTCTTCAGT TAAAGGAATGTGCTCCCTCAGGCTCTCT CCCATGGTGCATTGCTTCAGCACGCAGG CAGACACTTGTTCAAGCTAGGCTCCCTG TCTCCCATCTGTAGGAAATGCTTGGTAT GAAGGCCCTGGTGGACCTGGCTAGATG GGCAGCGCCAGTGAAGGGCTGTGTCT GGAGCCTGGGCTGTAATTAGTGGTTTGA ACTGGGTGCTCTGGGGAGAGGCAAGTA AGAATTTGCTTTCTGTTTTAGAGCAGGA GGAGCTGGCGGCTGGCTGTGCCTTAGC CGGCTCCTCGAAGAGCATTTGAGGTGTT CGCCATCTTAATGGGTTAAGACTCTCCT GTGCTAATCTGGTGGGTTGCTTTAGGC ACGGTGGTCCCACTGTGGTTGTGTGAAC AGTACCTTAATGCCAACACTTTGGAGGC CTAAGGTATCCCCATCTGCAGGAAGTGG GGTGCACA	p001075	D	--
270	IM000888	GATCCTCACACAAATTGAGTAGTACTAAC AAGAGTGTGATTCACATAGTCAATAAAG GTATAGGCCATCTGTGCCCTGGCTTGAC CTCCGCAGACCAGAAGCTAACAAAACCA AAACAGACTCAGTTTCTGCATGCTAACTT AACCATGATTTTCCAGACTATTTCTTTTAT CCTGTGAAAAATATATTAATCTCTATTCT GCAGAGTATCCCTTCTTTAAGAGAACAT GATTTCACTGTTTTTGACAATATGCCTAG ACACAGAAAAAATCATTTAGTTT	p001078	B	AA79335 6
271	IM000889	TTTTGAGTGCTCAGTGAAGTACTTAGGG CAGCCTAAGGAATACAGTGACCCACCAG GAAATGCCTTGTGTTTTGGCAGTCTGATA GCATCACTCACAGCTGTCGGTCGTGACT TCATTGGATC	p001079	A	Edar
272	IM000890	GATCCAGGGACAAAGAGCCCATCTCCT GTTCTTCGTAT	p001081	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
273	IM000891	ACTTTCAGGCAAGCTCTTTGCTCAGTGA ACCTGCTACCACACACAGACTCCTCCTC CCTGTTCCCGTCGTTAAAAAAGTTTAT TTGAGGTTTAGAGCAATGGCTCAGTGCT CAAGACTACTTGCTGTTCTTACAAAGGAC CTGGGGCTAGTTCCAACACCCACATGAT GGCTTACAATTCTCCAGTCTCAGGGGT CCAGAACTCTTTTTCTGGCATTGAATGCA CATGATGCATATATAGACAAGCAGGCAC ACACACACACATAAAATAAAACAAATCTT TTGAATGTAATTTTAAAAAGATTTATTAAT TTTAATTTTATGTGTATGAATGTTTTGCCT GCATGTATGTCTATGCACTGCATGTGTG CCTGGTGCTCAAGGTGTCTGATAGCCTG GTGCTGGGCTTGGTTCACTCAACAGCTG GCCCTATGAAGGCCAGCCGTGAGGACA CCTATCCATGCTGACAGACACAGATGCT CAAATGAGACAGCCCCTTCTCTATGAAT GCCCTCTTGAGAATGAACAACCTCCCTG CAGCAGACCTCCTTCTGGATACCCTGCC CTTCCATACTTTCTGGGTGTCTAGTTCTC TTCC	p001082	R	--
274	IM000892	GATCACACGCTTCACCTAATTACAAATGA TTTCTTTAGAGGGGTCTGTATATAACAGA GATGATAAAATTCAACGGCAGCCCTCCA ACTGCATTGATATACAGGAAGTACTCATG AAATTGGAGACACTGATTATCTCTTTGTG TGGTGTCCACATATGTGCCATCATATCAT ATTATTATTATTACATGGCTAAAAAATGG GGTCATAGGTTTCATGACCAGAACCAAA ATATTCCCCTGTAATTTACACAGGATTGA TGGTAAGAAATGAAAACAGTTTACATTTT TGATAATTTACTTACTTGACATAAAATGT GACTTTTCATTTCTTGCATTCTTTTCAC AGGTAAGGCTACGACAATAGATTCTCAG TTCTCCACCTCTCTCTATCTTGTCTACTC TATCAGCAGCAATAGCAACAGTTTTCCAT GGTCCCTTCCATCTGTAAAAGCAATAAAAA ATAACAAAGAAAACCATACAAACCATTAG AATATGAGTTGGTATTCACAACTCTCCTC TCAATACTTCATATTTTAAAAATTACTAGA AATATTCATCAATAATTTTCATTTGTTAG CTCTAGATAATGTTTCCAGG	p001083	D	--



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275	IM000893	GATCATGGTTATTTTTGTAGGGTTTATTT ATACATGTCTACATGAATTTATGTGCACC AGATGTGTGCAGGTGCCCATAGAGGCCT GCGAGGATGCCAGATACAGATAGTTATG AGCCACCTAATATAGATGTTGGGAATTG AACCCATGTACTCTGCAAGAGCAGCAAG TACTCTTAACTACTGAGTCATCTGTTTAG CCCTCCTGTTGGGATTTAATGGTCAGTG TGAAATACTATGAAGATAGAAGGGTTTCC TAGACTCTGGTGTGTAGGGGTGGGGTAT CTGTGAGATGGGTAAGCTCTGTTGGCTT TCTAAGAAGGAGAATGAGCAGAAGGCAC ACATAGACATTACACTTTCACACACATG CATGCCAAACACCACACATGCACACCAC ATACCACACGCGCCCTCCTGTTTCTTACT ATGTAATAATGTTCTTGTAACTTAGTA CTCTGCTAATGAAAAGGTCACCACTAACT AGATGCTAGCCTTCAACTTTGGACCAGA ACTATGAGCCCAAATAAACCTCTTGCATT TATAATTTAGCCAGCATGTAGAACTGTGT CAATAACAATGGAATAGTGTTG	p001085	R	--
276	IM000894	GATCATCTGGCTAAAATTTTATAATATGA CTCTTTAAATTCCTTAAGAATTCACAAGG ACCTTTATGTTGAAATTACTCATATGTAA GCTTACTGGAATGAGATGGCTCCCCAGT TGAAAACACCATTCTTAAATACTCAGAA AATAAGAACGAGGCCAGCCCGGTCTACA AAGTGAGTTCCAGGACAACCAGAGCTAT ACAGAGAAAACCTGTCTCAAAACAAAAA CAAAAACAAAAACCAAAAAAAAAACAAAA AAGAAAAACAAAAACAAAAACAAAAAAT GTAGATATAAAGAAAGATAGTGTGTTGCT GGAAATAAATAGTAATATAAACTTAACAG CAGCCTGTCAATTGCAGGGTTTTGCAC TTGCAGCTCAGAAAGAAGTGACCCTCCT CAGGAAGTAG	p001086	R	--

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277	IM000895	GTGGGTTGTGTGACTCAGAGAGCAAGCT TCTACCTCCACAGGCAAGGATGCCTGTG CACACAGAAATGAGATGAAGTCATATGT GGGGACTGGAGTTGCAGTGGCTCCCAG AAGGAGGTGTGCAGAGTTCAGGCTGGA GTCCAGATGAGGAACATCAAATAGAGAG GCCTTTGGAGGGAGTGGGTTCTCTTGAT AAGTAGGACTGCCACCCATATCAAGTAT AAGACTGCCAATCATACTGAATCTCAGG TTATTTCCCATGTAGCATTGGGAACATAT AGCATTGTGCACACTGCTATAGCAAAGAA TCTGTGATGAGGTTGGGAGTGGAGGGG AACGCCTTTGGTCCTAGAAAAAGAACCA AAGGTAGGCTGATC	p001087	D	--
278	IM000896	CCTGCCCTTGCCAGACCCGACCGCAGC TCATCGAGGAGGTACCCTCTAAAGTCGT CACCTTGAGGAGACAAGCTCTGTCATAG TGCTCGCAGCCCCGCGGCCCTGCGCC AGGTTGCGGACGCCATCTTCCCGCGCC GTCGCCGCCATCTCCTCCTCCTCCTCCT CCACCACCTCCCCCTCACCTGCCACTGA ACCTTTCCCCCAGCTTGAAGCCACGCC TTAAGGAAGCAGAGTCGGTCCGGACACCC GCTCCTCCTCAGAGCAGCGGCCACCAG AGTCAGGAAGGGGGGTCCAATCACGT GATC	p001088	R	--
279	IM000897	GCTCAATTAGTTTATTTAAATTCAAAACAA AGCTAAAAGCCTGATGTGTCAGTTGCCT TCAGCAGAGCTGTTTGGGGCCCATTTGTT AATGTTGTGAATTAAGTTCTGATGTAAGT AACCAAGCCACTCCCCACACTCTTACTT GCAAGAGTTCCAGGCAGATGTTAAGGTC AACCCACCTGACTCTGATC	p001089	D	--
280	IM000898	GATCACAGTGTTTATCTCAGCAACAGAAA GCAAATGAGGACACACCTGGGTCTCACT GATATACTTGGTGATATGTGTAGTTATTA TGTCTCACAGTAATTGGACAAGGAAGAG AGTTCATTGTTTTAGAATGTTGTAAGTGG CATTGTTCTTCTCTCTCTTGTTCATAAA ATCTCACAATATCTACAGCTGTGAGGTC CAAGGGGCTCATTGGTGATACCCACTCT TTCTACTTTGTGTGACCAACCTCTTTTGG ATGTCAAGGGT	p001091	C	--

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281	IM000899	GATCAGTTGCTATTGCTTGATTGATTGCG AGACTTTCTTAACAAGAGTCTTTGTCTCC TCTCACTCCCTAGCTTCATCTTAGAACTT AAACCCACAGCCCAAATGAGTAGTTGTA TGTCATATGCCTCGGCCAAAGCACGACT GAAAGGAAAAGAAAGGCAGACACTGGA GTGCAGGAAGAAGACACAAGGCAAAGC CCAGAATTCAAAAGTAGAAGCACAGATT GTTTTCTTTGTTT	p001092	C	--
282	IM000900	GTACCCCTGCATCCCCGGTGTGGCCTTGG AGTCTGATGCCAGCACTACAGAGCCAAG CCATAATACAAACCAAATAGAATTAACAA GAGCTCCATATGATC	p001093	D	--
283	IM000901	GATCACCTTCCTAGGATGAACGAAGAAG GATGGCTGGAGTTAGGGACCCAAGGG ACTTCCCCCTAGAGCTGGCTGTGTACCC TAGGCATGTGTGACTGCAGCTGTACAAG CAGGGTATTCTGGGATTCACAGTCCTCA GGATAAGATGACACTACAGATTCTAAGC TTTATACCCAACATGGTGGAACCCCATG GTCACACTCTTTCACAGATGGTCACTCC CATTGCCCCAAGCCCAGCCTTTATCCAA G	p001094	C	--
284	IM000902	GATCAATAACAGCAAAAAGAAAAAAGAA GTTTACTTTTCATGTAGCAATGTGGATAA TTCCCATCCAGAGAAAACAAAACCAAGTTC CAG	p001095	C	--
285	IM000903	GATCAGGGAAGATGTCACCTCCAACCCA GCCTAGACATGGTGCTGTGACCA	p001096	D	--
286	IM000904	GATCAAGGAGCAACCCAATAGCTTCTAT TCCCCCCTACTAAAATATGACCCACTG ATGGATTCTGGGGATGCACAGATGTTCT CAGAAGTTACTGATGAACACACCATGCT CTAACAAATAGTATCAAACCCACAGTCAC AGATGGCCCTAGTTAAGCACAGTGCATC ACAAAGCAAAGCAAAGAGCCTTGACTGT GGGAAAGGTACTTGTGGTGAGGACTAGT GGGGTATGAAAGAAATTAGAGAGGATGA AGGTAGTGATATTCAGTGTGTGTGTGTG TGTGTGTGTGTGTGTGTGTGTGTGTG TGTGTAAGACTATTAAGAACACCCTTTT TTAAAGAAAGGCTTTCTTGAGTGTCAAC	p001097	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
287	IM000905	GGTTAATAAGCTAGATTATCGTGTATATA TAAAGTGTGTATGTATACGTTTGGGGATT GTACAGAATGCACAGCGTAGTATTCAGG AAAAAGGAGACTGGGAAATTAATGTATAA ATTAAAATCAGCTTTTAATTAGCTTAACA CACACATACGAAGGCAAAAATGTAACGT TACTTTGATC	p001098	K	<i>Myc</i>
288	IM000906	GTGAACGACAGCAGAATCGGGTTGTACC TCAAAGCACTTACCTTTCCCAATACACCT GATC	p001099	D	--
289	IM000907	GATCAGTGACAATGTAGCTTGCCTGGA AGGATACTTGAGTC	p001100	D	--
290	IM000908	GATCAGCAAAATGGGACATCGAAGTTGA ACCAAAGTCATAATAAACATCCTGAGGT ACATAAACACTCTGTAATAGACTAATACA GTTCTCCAGGCACCAACAGAAACCTTG ACTACTTCCCTTGACTACTTCAGTCAAAT CTTCTGATAAAACCAGACCCAACTTGGA AACGTCCATGTATACAATG	p001101	D	--
291	IM000909	GATCATCTGCTTCTACCCCCAATTAAGG ACGGACTAAGAACATAAAAAGAATCCAG GCACCTAGGTTTGCAGAAATCTAAAGGT TGAGTTCCTTT	p001102	D	--
292	IM000910	GATCACAAGTTATAGTTGAATAACAAGTC CTGTGTGTGTCTATGTATCCGTATATCAT ATTTTCTTTATCTGTTACTCTATTTCATGGA AACTAGGTGGATGTGTTAACTTGGCTATT ATGAGTTTTGCTGCTAT	p001103	D	--
293	IM000911	CTACAATGGTTCAGGCTTTGGAATATCAC TCTATAGGCTGTCTGCCGGCCACCACCC TTCAGACTGCCACTCACAGGTGCCCGTG AAGGCTGCCGAGAGGCAGTCCCCATCA GCCTGTCTCCTACACCCACACACTCTGT GTGGAGACCACAGGCGCCCAAAGGGTA TGCTAGTCTCTGCTCTACCGCGTACCCT CTCCTGAAGGCAGGCATTTTCAGAGATTC CAGTTTCACCAGGAAGCTCAGATC	p001104	C	--
294	IM000912	GATCTTTTCCCCCTTTGTAGTATCAGAGA GAAAAGCCATGGCATGCATGGCACATGC TAGGCAAACACTCAAGCATCCTACTCTG TGATGCAGTTTGAAACAACTTTTTTTTT CTTTTTCTTTCTTTTTCTTTTTCTTTTC TTTTCTTTTTCTTTCTTTTTTTTTTTTT TGAGT	p001105	R	--

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295	IM000913	GATCTCTCCCATCCTCCTGTTGCCTCTT GTCTGTCATACCTCTACTACTCCATCAGT TTGCTGCCTCTGAGTCCCTCTTCTCCTC TCCTATCCCTCCTCCCATCTTCCTCATCT CCAGGTCTCTCCAGGTCTTCCTTCTTCC CTCTTTTCTTCCCCTTTTCTCTTTCCACT GTCTTGATTCCCTTCTTTCTCTGTTGG TCCCTTCCCTCGCACCTCTTTCCTCCTGT CCCTCCTTTTCATGTACCATATTTCTCTT CCTCTTTCTGTGTCTCCTCTTTCTTCTCCT CCTTTACTTTCTTCTAACCTTCCTCTTTC TCCTCCTCCGGCAAGCCTTTGCTT	p001106	A	<i>Gata1</i>
296	IM000914	GGTTGTTCCAGTTAAATTGGCTCTCTACA GGAACATGGCTTAGTTCTCCCTTAGCCT TTCATGACCCTACACCTCAGACACTAGT CAAAGTCTAGCTTAATAAAGTGTTGAGGA TGTTGGTGGAGGGGGGAGATTGTTAAT ACAGATC	p001107	D	--
297	IM000915	GGACCACTTTAGTATGGGTCATATGTTCT AACTTTCTTTCAATTTCTTTCCAT CTGCATTGATTGTGCCAGTTATCATTAG TGACTTATTTTAGTAACTTAAGGGAAAGT TGTCTATGCTCTACTTAGTGTGATTTAA CTTACTCTCCAGACATGGGAGTGCTTATT TTTGTTCCTTACCTCATCCAGGAGCTT GTAGATC	p001108	D	--
298	IM000916	GATCCGATTATGAAACCGGTTTGAAC	p001109	D	--
299	IM000917	GATCTGTGGAATGCTATCCAGCTCTTCC AACAATAC	p001110	D	--
300	IM000918	TTAGTATCTGCATCTGACTCTTTCAGCTG TTCGTTAGGCCTTTCGGAGGGCAGCCAT GCTAGGCTCCTGTCTGCAAGCACACCAC AACATCAGTAACAGTCTCAGGGGTCTGA GCCTCCCCCTTGAGCTAGATC	p001111	R	--
301	IM000919	GATCTGTGGTAATGATTCTGTAAATACAG ATAAACAACGTACACATGGGAATTGTTCC CTGTGTGAAAGTGTTTCATCATAAGGTGTT TTTATTTTATCTACAATATCTTTGGGTTTT TAG	p001112	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
302	IM000920	ACTGCCACATTCCCTAACACCTCATCAAA GAAAACAACACCACAGGTCTCAGGCTGC CACTCTAGACCTCCGAGTTGACTCTGGC TCCTGCTCTCTGCAAGCAAACACGCATC CCTCAAGTCTTCATGCTGGTTCTCTCAAG TCTTCATGCTGGCTCTCTGTAGTTCTGTA AGCTTACCCTTTTCAGTGGTGATTGTTGGG AGATC	p001113	D	--
303	IM000921	GATCTCCTGGCTTTGTAGATAAATGAAGA GAGTTCGTTACCAACTGAACTAAAGAGC GGCACAGGAAATTAACAAAAACAAACAA ACTGATAGTTAACTCAATTGAGTAAGTAT GGAGTTTTGGGACCAAGACATATTAGGC AAACAGACAGTTTAAGGCCTAG	p001114	D	--
304	IM000922	GTTCTGTACTTTATCATGTCTTACCCCT ACCTCCCTCCATTTTAATCATCTTTACTG GGATGTAATGCATTCTTTGTCCATTCCA GGATGCTATAACAAGATACCTTCAGCCT GTAAGCTATAGAACAGTGTGGTCCTCAA CCTTCCTAACTTTGTGACCCTATAATATA GATC	p001117	D	--
305	IM000923	CCANCGTGCCANACTCANAANGGAATTT TATTCATAGATTCTNTCANACTGCTGTCC CACATGTGTTCAAAANCAGGTAGGTCTT GTCANAT	p001119	D	--
306	IM000924	GATCTCATTGCACAGAAGAGTTAGAAGA AAGAAAGAAAAGCAGACTGGGAAAAATT TTTGACGCGAGCATTGAGAGATTGAACA TCTATCTAACTTATGCAAAATTCCTATCA AAAGAAAAAAAAGCTTCAACAGCTGGG TAAGTTAAATGTAAGTATAAGGCAACAC AAGGCAAAGTGTTGTTCTTTTGCTTGTT TCCGAGATGAGCTCAATTAATAATCAAT AGCGACAACAATTCTGAGCTGGACTAAC AAAGAGTAGAACAATACTACCCAACGCT TGTGGTTAGGTAACCTTACACAATATTTT CCTAATGCTATTCGGCAATAATTGTCAAG AAAA	p001121	D	--
307	IM000925	GATCTTTTCTACAAGACTTCTGGGTGAC CTTGCCAAGCCCAGCCACTGGCTGTGGT ACCTCACCAGGACACTCGGTGGACATTA GGTAGTGCTCCCCAAGTGCTAGGTGACA GTTTATGCTTCAAAGTGACTCCTGCAC	p001122	D	--

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308	IM000926	GTGCTGACGCGCCCTTGCATTTGGGAGA GCAGTCAAGCTATCTGTACCTTCACCGT AAGACTACATTGTCACTGCTGGCTTCCC TCCTGTGCAAGGGACGCATTTGGGTCAG ACTATGCATGAAACAGGACAACAAAGGT AGGGCCATTGGTAGATC	p001123	D	--
309	IM000927	GATCTCACTGAATATAAAAAGACATCAGT CCAAGGGTGGAAATTTAACCAAAATAATA CAATTGTTGTTG	p001124	D	--
310	IM000928	GATCCTCCAGGAAGTAGAGTTACAGACA ATGCCCCGCCTTGTATT	p001125	D	--
311	IM000929	GTGGCAGTGACTGTCCGTGTGGGAAAC GTTTAGCAAGTCCGAGCGTGTTGATC	p001127	K	<i>Nmyc</i>
312	IM000930	CAGGAGAGTGTCTCAAAAAGCAGCAAAG CACCCAGCACCTTAGGGTGAAGGACCAC TTCTGGAATGTATCCTCCAGTTGCAAAT GTACACTGTCTCATTCACTCCTGTGACAT ACTTTGTTTGTGAATGCTAATATCACATA GTTGATC	p001129	C	--
313	IM000931	CCAGCAGAGACCAAGCATCCAAAACATG AGCCCATTTCAAGGCTTCAACCATAGCAG CTCCCATCTCAATCCTGTTACCCCCCA CCCCACCCCCCGCTTCTCTATTTAAATCA CCTCTCAGTGACCAAAAAGATGCTCA TGGCAAATGGACTCTTGGCTCTCTTTTAC CTAATACTGAAGGTAACAAGATAATCAAC TGTTTCCTCTCCTTCCCGGGGACCTCAT CATACAACATTCTCCACATGAAATTATC ACCACGTCCAATACCCACATCCTCCCCG TCCTGTAGAGAAACCATGCCTAGCAG CAGTGGTTTCCACCTCTGTGCTCCCTT CCACCTCGATC	p001131	D	--
314	IM000932	GATCGCTGTGGTTGGTGTCTGTGTATAT GCACTGTACATACTAACCAGGTACACAC ATAAATATTTAATATATAAAAAATAAAGTG CTTTCTAAGAGGCCCTAGGCAGGGACG TTATAAAACATTTACAAAAGCAGCAAAAC AAAATTGATACAATCAAAAAACAACACT ATAACCAACATAGGTGAAAACAGCCAAA CACATAATGTACAATCTGGTGTTCAGG ACAAACATCTGTGATATACATGGTATATA CATACATACTTTTCACTCAATAA	p001132	B	Mm.3669 2

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315	IM000933	GATCGCTAAGTGTGCGCGGCCGCGCTC TGCAGAATGAATGGAGGGAATGAATGAG GGTGC GCGCGCCCCGAGGCCCGGCTTGC GTCAGCCATGCGTGCCCCGGCATGGACA CGGCCTGGCCTTCCTGGGAGGATGGGA CCGGATGCAGTTAGTCCAGGCGTTCAGC ATCCCAGGGCCCTTCCTCTGTTGCGTGG TCTGAGTAATCTGTCTCGCAGAAGATAC CCT	p001133	B	Mm.1515 28
316	IM000934	GGAGGTCTCTGTAGGTGCTTAGACTCAC GTTACAGTCATTCCAGAGGAGGGAGCTG CAGCTGCTAGTTTCTGTGCACACCGATC	p001136	D	--
317	IM000935	GATCGGCTGTCAAGACTGGGGAAGGGT CCTCCTAG	p001138	D	--
318	IM000936	AAGCAAGAGGTAATAAAATACATGTGGA TGGATGACTCAGGGGTTAGAGCATACA CCGATC	p001139	D	--
319	IM000937	GATCGGGGACCTTGCATAAAGGGGTCCA GGGCTCTCAGTCCTTGGGAAGG	p001140	B	AA70964 7
320	IM000938	GATCGTGATGACTTCATAACCATCACGT GTGAAAAGACTTAATGGCGCTGAATTCA CATGACACTTAAATGCACAAAGTAACAA ATTTTATGTCACATGTATTAACTACAGC TAAGTACATGGGGAAAAAGTTAGACTTA GAATAACTCATCCAGAGTCATATGGTAG	p001141	C	--
321	IM000939	GATCGAGGAGTAACCCAATAGCTCCTAT TCCCCCCTTACTAAATATGACCCACTGA TGGATTCTGGGGATGCACAGATGTTCTC AGAAGTTACTGATGAACACACCATGCTC TAACAAACAGTATCAAACCCACAGTCACA GATGGCCCTAGTTAAGCACAGTGCATCA CAAAGCAAAGCAAAGAGCCTTGACTGTG GGAAAGGTACTTGTGGTGAGGACTAGTG GGGTATGAAAGAAATTAGAGAGGATGAA GGTAGTGATATTCAGTGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGTGTGT GTGTGTAAGACTATTAAGAACACCCTTT TTTAAAGAAAGGCTTTCTTGAGTGTACCC	p001144	R	--



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322	IM000940	GATCGGGCCACATCTCAGACACTCCTAT AGCTACAGAGAGATACCGTTTCCTGTTAT CTTTGCAGACAACTTTATCTGTTACTCAG AGAAAACCTCCAGGTGCCCCCTAAAGAAA CTGGGCCCTACATCACATACCCATACCA CACACATGCAACATGCAAAACATACACA CATACATAGACACACACACCACACGCAC ACAGACACATACAGACACACACATAC TATACATACAGACACATATGCTACACACA TACAGACACACACAAGCACACATACTTC ACACACAGAGACACACACACCACACACA CACAC	p001149	R	--
323	IM000941	GCCTGCCTCTGCCTCTCGAGTGTGCGGA ATAAAGGCGTGCTAGAGCCTTCACTTGG CTCTCTCTCTCTCTCTCTCTTTAACC TCCTTTTTCTTTAATGAGTTATTTATTT TATTTTATGTGCATTTGTGTTTGCCTGT ATCCGATC	p001151	R	--
324	IM000942	GCTTCAATATTCGAAAAGAATTAGTAAGA AAGGCTGTTCGATC	p001152	D	--
325	IM000943	CTACCAGGAAGTCAGGGGTTTCCAGGAA CCCACACTTGGCTTCCTCTGCACAGAGG GACCTCATACCAGTGAGATGGTGATATG CTCCCTTGTTCTGAGCCTCAGTGGAAG CGACTTTCTATGGATACTCCCTCCCTCGT GCCTCTCCTTCTTCCCTCTCTGCTCTCC CCCCCCCCCTCGCCCTCACGATC	p001154	D	--
326	IM000944	ATACACACCATCAGATATACCTCATTCTG ATATACCTACAGGTACACCAATCACACAC ACACATTTACTCACATGTACATGCACACA CCACATCGGTTAGAACCAAAGACCTCAC ACACACCCCTCACACATGTTTCATCTCCA TTATCAGTGCCGATC	p001155	D	--
327	IM000945	GATCGTCAGGTTATGAATGCCAT	p001156	C	--
328	IM000946	AGTTCTCAGAACCAGCTACTGTTTACACA GGGCCTCATGCAGCCTTGCTGTCTCCTCA TTCTGCAAGCACAGGATACACACCCCTG AAGGCCAGATTGTCAGGTCAGCCCGATC	p001157	C	--
329	IM000947	CTTCAAACCGGTCCTGCGAGGAGTCCAC AACCTCTGCCTGCCGATC	p001158	D	--

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330	IM000948	GATCGAGGCCAGCCTGGTCTACAAAGTG AGTCCCAGGACAGCCAGGGCGATACAG AGAAACCCTGTCTCAAAACAAACAAACAA ACAAGATTCCATTGAGGAACACCCAGAT GGAGACATGGGTGTTCTCCATAGAAGGG TTAGGGGCTTCCACACCGTTGACAC	p001159	B	Mm.8136 6
331	IM000949	GATCGGTGTGCTTTCTGCAGTTTCAGCG AGGACTCTGGGCCCAAATGTTTTAAAG CAGAAAATTGGTAACACTAGAGATATTGT CAAAATACGATTTCTCTGGTTCAGAAAT GGCGAGAGGGAGGGCTGGAAGGGTGG AGTGGGAAGGAATTGTCATCAAAGCATT GTTGATAC	p001160	B	AA40894 5
332	IM000950	CTGTCTCAGGCATGAAAACACTAAAAGA TGACCAATTTCAATAAAGATGACCTGAAT GTCTACTCAATTCACACATAAGGTCTAC AAGATGTAAATGGGCCGATC	p001161	D	--
333	IM000951	GATCGTGGAACAGAGCCTTGAATATAA TGAAGAAACAGAGGGCAGGCAGCAGCC GCAGCACAGCAGGGGCACTGTGAGCAG GCAGCAACAGGGGG	p001162	D	--
334	IM000952	CTCCCTACTACCTTCCCTTCTGGACNT CCACTGAGATGAGGCAGGATAAAGGGTC AAAAGAGACCTGACCTTCTTGCCAAAG CCAGGGATTTCTGGAAGAATAGAAATGG TTCTGGAATTCACAGATGCAGTGGTCTA GGATC	p001163	C	--
335	IM000953	GATCCATAGGTCTCTGCTTTCCCATTC GGGCTGGAGTTATAGATATCTGTCTATC ACCCAGCTTTTATGTAGGTTCCAGG	p001164	D	--
336	IM000954	TATGTATCTACAAGCCAGAAGAGGGCAT TGGATC	p001166	D	--
337	IM000955	GATCCGAGTTCTCTCCGGCCACGTACCT TCACATCCCATGCACCCTGGTATGTAAG AAGAGCCCAGCTCAC	p001167	D	--
338	IM000956	TCCATAATATTTCTCAGAAGGATC	p001168	D	--

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339	IM000957	TATAGTTCTGCCTGTGGAGTGTGAGCAG AAATGTGTATCGTTTCTGGGTCAGAGCTT TCAGGAAGTGAAGCATGACTGCTCTACAG TGTCCTTCTCCTTCTGCCTGCTGAAGCC CTAGGGGACAATAGAACCACAGGATGAA AGGACTCGGGATC	p001169	D	--
340	IM000958	GATCCAATGGCAGCTAGCAGAGTCAGAG AGCCCTCACTCCAGTTAACTAGGGGACC CACATGAAGTTCAAGCTACATATCTGCTA CAAATGTTTGAGGGACCTCCTAGCTCCA CGCCACATGCTCTTTGGTTGGTGGTTCA GTCTCTGTGAGCCCCACTGGGCTCAGGT TAGTTGACCTACAGTCTTCTTGTGGTATC CTTGACCCCTCTGACCCCAAGAGTTTAAC AATAGGCCTTCTGACTCTAGAAATCTACC TACATTTTTTCCACTTTAAATTCTCTGGC TCACATAATACCAATGAAT	p001171	R	--
341	IM000959	GATCCATCTGCACAGTCTGTCACCGGGG TCCAGCAAGTAGCAGCCTTTCTGCTGCT GTCTGTCAGACCCTCCAGGGAGGGAGA GCTTGTCTTCTGGCCTCCCAACAGGACC CTGCGTGACGATGCAGGGACAGCAATG ACAACTCATTCCAGACTCCAGGTCCCTG GAGGAGCCTCCCACAAGGGAAGAGAC TACTTCACTGGTCTGGGCCCTCTTTG CGCGCCCCGCCCCAGACTCAGCGTCT AGTGTTGCTGGGCTCCCCT	p001172	K	<i>Pim1</i>
342	IM000960	AGGGTAACAGGCTTAGTTTGGGGCCTTT CTGTTACAGGAAAACCATGAAATGTCCT GAAGTGCTCAACAAACAGGGAATATAGA AAATCATAATGGTTCTCCTAGCACAAAG GAAGCATGTTAAAAATTGCAGCAAAATA AAAAAGAACAGATTCTTAAGATTGAGGG ATTTTACGGGGTGGTACTTTTCTTTCTC TTATAAACATTTATTTACTTTTGTATTCA AGACAGGATC	p001173	D	--
343	IM000961	GATCCAGCTGTTTGCTAACATACGTAAA GGTATGGATGCTGAGAGAGTATCTATCG AAAGCGAAGGCACCCTCCCCAAATTCAA GAAAGCAGCTGTTTCTAGAACCAAAGAC ACCACCGCCGCCGCCGCCACCACCACC CGCGAGCGCCCGGACCCTGTTACAGAG TGTC	p001174	C	--

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344	IM000962	GATCCTGAAATTATCACATTTGAATCAAA TCATGCCCTGCCGAGGATAAATAACCCA AACGACCGAGAAAACCGAGAAAAAGAAC ATTACTGACCATCCTTC	p001175	D	--
345	IM000963	GATCCAGTCCAGAGCAATGTTACGTCT GTGATGGTAT	p001176	D	--
346	IM000964	AAAGGTGCTCTCAATACTTAACAATCCAT AAGCTTGTGCTCTCTTAGTCGTAAAGGT GGGGTCCATCAAAATCCCATGACACCAC AGCGAGACCAAACCTCTTTTCTTACTC CGAATCACCCATCCCATGTGGGAGACGA ATAAGAACACAACTACATCTTCAGTGAC ATAGAGTAGCATCTGCAACAGAGGAAGT GGATGGAGACCTTGTCTCTGGTCAAAGA CAAAGCATGTGACAGCTGAGCCTGGCAC TTCCTACTTGGGTCACAGCTCAAACCCA CCTGAACCAACAGCAGAGCCCCACAGG GATGGGACTCACATGTTCCCTCTTGCC CTGGAGCTTCGTGCATGTTGTTAGAAGC TAACTGGCTAACACGCACGGGAACAGGC AATGTAGTTGGAGTATGAATCGAAGTCA CTGGGCATGGTCCTCAGTCAGCCAGGAT C	p001177	C	--
347	IM000965	CTAGACTAGTATGGCAGAACCTATCTTCT TCTAATCATTTAGATGAATACTCCACATG AGAGAGCCCTGAGAATATCTGTAAAAAG TAATCCAGGTTCTGTTACTTCTAGCTAAT CTTATCTAGGTAATAATAGATAAGGAATC GGGATTCACGAACACAAATACCTGTACA AAGCATGTTGTCTCACACGGGACGAACA CTGTTTCTGCTGTGCTTTATAACGCTGG GACATACAAAACCTAGACTCTGCCTAAGA AGTGTTTGGAAACATTTGGGTAAATTAT AGTCAGATAAAACAACAACCATGAGTAAA TCGAAGAATATAAACTAGGGATC	p001178	C	--
348	IM000966	TTTCCTGGACAATAATGTTTTCTTCATTAA ATTTACACTTAGAGCATTGTCTTAATCCA TGAATAATTCCCAGCTCCTAGCTCATTAC CTGTGACACAGCAGGGATTCATACATTT ATTGAATGAATGGATGAGTGAATGAATAA AAGAATGAGCATATCAAGAGGATC	p001179	D	--
349	IM000967	GATCCCTTCTGTCTTTGGTTATCTC	p001181	D	--

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350	IM000968	GATCCACCACTGAGCCACTTCTTCAGCC TGTGACTGTCATTCTTAATCATCCACACA GACTTCTCCTTGGCAGATTTTGCCCACC TCTTAAGACTTTTACAAAGGTTTTTTCTT CTGCAGGGCACATGAGAAAACAACTCTG TCATAAAGAAACCCAGGAAGAAAACCAG CAGAGGCAGGTGAGTTAAGCCTGTGGT GGACATTCTTCTGGGGATGACCAGATG GGAACAGTAATTCACAGAGGCAGAGGG GTCTGCAGTCACTCTGCATGCCACATGT GTAACCCCTTAAGAAGTGAGGAATGCTCT CAACAGGAAAAACACAGCAGCAAATGCT ATGATACCAAAGCCACAACTCCATGGGT CCCTGGAGCCTCTCGAACTAAGCTGCCA GCTAGGGAGCTAACACTAGCTTTGGATG AAACACAGCTCTGGTAGAGTT	p001182	C	--
351	IM000969	GCTGGGATTTGAACTCAGGGCCTTCAGA AGAGCAGTCTGCTCTTACCCGCTGAACC ATCTCACCAGCCCCCTCCGTTCTTCCTT TCTTCCTTCCTTTTTTTTTTCCACATTGTT TTCAGACTGCACCTTGTTTAGTAGCTAG GCTGGCTTCCAATTCCCAATGATTGAG CTATGGGTATACTCTCTTCACCTACTTTG ATTTTTGTTTGTTTATTTGTTTTTTGTTT TTTTGAGACAGGGTTTCTCTGTATAGCCC TGGCTGTTCTGGAACCTCACTTTGTAGAC CAGGCTGGCCTTGAACCTCAGAAATCTGC CTGCCTCTGCCTCAAAGTGCTGGGATC	p001183	R	--
352	IM000970	GCTTCATTTAATATACATCATTTACCAGA AACCACAGACATCTTTGTACCAACATATA GTAATATTAATCACAATAGCCATCACTCT TATGTAAGGATGAGAAGACTCCCAGCTA ATATGCTAATGTGTAGAAGATGCCAGAT GGATC	p001184	D	--
353	IM000971	GATCCCTGCTTCTGTAAATCCGCAACGA CAATTGTTATCTTCTCCTTTTCTTTCTTT ATTTGTTTTATTCTATTTATTTTTCAGAT GAAAA	p001185	C	--
354	IM000972	GATCCTCCTGCCTCTGCCTCCTTCAGCA AATCCTACCGGCGTGCGCCACCACTACC GGCGAAAAA	p001186	R	--

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355	IM000973	GATCCCCCTTTCTCTGTCTACGGCCT CTGTCCTGTGTTAGCTGTAGGCCTACTC TGTATGAACAGACCTCAGCGGAGGGGT TGGACTTGGGCTTGTGTTTCTTAAGAGA ATGGGGCTTCCATGACTGTCCCTCTGTC CCTTTCATCCTAACCTGCCTCCCGCTA ACAGGCAGCCTGTATGTTTCTTGCACTG TTCCTTCCTCCTGACGGTCTGAGTCGTTT CCCTCAGAGACTGTTGCTGCTGCTTCAG CTTTCTCTCAGCTTCTCTCAGGGCTTCC GCTCTGGAGTTTCTCCTGCTTCTCTGTTT ACTTTTCAAAGCTCAGCCTCCATCTTCTG CACCTGCGGAGTCATCACTGATTCCCAG CTGTGGCCTGTCACCCCTCCCTTTCTTTC TTCCTCCTGTGCCACCACCATGCACCCT CCCCTTCTGTCTGTTGTGTTGTCCTAACCT TTTCTTCTCCCATGCACCCTCCCCTTCT GTCTGTTGTGTTGTCCTAACCTTTCTTCT CCTCTCTGTGCTCTGCAGGTTTAGGGT CTCTGTATGATTTGTACCTGCATTTATTT GAACCTCCACTCTTCTCTTCCCTCTCTT ATC	p001187	D	--
356	IM000974	GATCCTGCAATACCTCTCCTGGGCATAT ATCTAGAAGATGTTTCAACTGGTAATAAG AACACATGCTCTACTATGTTTCATAGCAGC CTTATTTATAATAGCCAGAAGCTGGAAAG AATCCAGATGTCCCTCAACAGAGGAATG GGTACAGAAAATGTGATACATTTACAA	p001188	R	--
357	IM000975	ATCTAAACTATAATAGTTGCAGGGCTAGT TCATTGTCAGGTGCGTGGCGAAAGAGTG CAAATCCCGGGGGTTCTTCTTCAGAAT CAACGAGGCAATACACTTGAACATGTAT GTTTTTGTAACTCTGCGGGGCATCACCCG TCCTCCAGGATC	p001190	D	--
358	IM000976	GATCCCCCAGAAGTGATAGTTTAACAGT GAGGTGAATGCAAGCAATAAGCTACCTA AATCATTAACCTTCTATTTTATTAGCAT CTATTAGTTGCACACAGCAGTGATGGGT TTCATT	p001192	K	<i>Irf4</i>

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359	IM000977	GGACCTCTGTACAAATGTCGGGAGATAA GGGAAGAAAAAGACGACAGAGATAGCA GTCAGGATGTAATGTGTACTAGATGAGT GGTTCAAGCAATAGGATGGAAAGGGCTT AGCAGGAGAGATTTTTAAGGATGGAGGC AGTAGATTACATCTGGGAAATGTCACTG GAACTGGATC	p001194	D	--
360	IM000978	GATCACCAGGCTGGGCAGGCCACCTAA GGAAGTGGCAGGGCACGGGCACTTCC CCAGAGCACCTCTGGGCACTCTGAGA GGGGCACAGATGTACTGCACTAGGCTG GGCCCGGAGGAG	p001196	D	--
361	IM000979	ATATAAAATATCGAACGTCCTCTGGCTTG TAAATATCATGTAAACCTTCAAAGCGTTC GAAAGCGCAGGAAATCTGAGTCAACAGA ATAGTATGTAAGTTTATTTTATAGAACCT GCCTGAACTGCAAGGGAGGGGCGGGGC GTGGACCCAGGCCTGCCTGCCAATCTG CGCTGCCAGTGAACCTAAGCCTGATC	p001197	D	--
362	IM000980	GATCAAGTCCTGGTCAGTACCAAGTTAA AAAAAAACTATATAAAAGCTATATTAGG GGACAGCTGTGGCTTTTGTAGAAAAGAA GGTCCTGGTGCTATGACCTGCAGATGCC CATGTGGAAGTCTTCAGATGAAGACTTT CTCATGGAGTAAACATACTCTGTTGTTTG ACCATGTGGACTTGGTTCAAATGCCCA TGGATGCTCCTTTGGGTACCAGGCTTCA GTGGGAGTCCCAAGCCCATGTCTTTATT TGAGCATGAGCAGTACTGATGCTTACCT AGTCTTATTCTTTCCTTGCCCCCTGCCTG GACCGTCTCTGGTTACAAGGATGCTGCA GTGGGAAGCGGTATGACCGTTACCTTTA TGGGACTGAGACCAACTAAGGGGAGGC TGAGGAGGCTGCAGTGAAGTTATTGTTG GGACTGTGGGCTAAGATGGAAGATAACA TGTTAACAACTCAAGTGCGGAGGTCTC AGAAGTAAAATTGCCTGGTTAGTA	p001200	D	--
363	IM000981	GATCAATTGGTAACCAAGCCTTGAAGTG AAGAGTCGTGAGGTGGGGGACTTTATAT	p001201	D	--
364	IM000982	GTATCTCCACCTGGCTCAATATAGGCT CTTTTCAAAGGCTAAATTAAGACCAAGGA CACAGAAGGGTAGCTCGCTGGGCAAAC GTGATCCCTGCTGATAGTGTAG	p001202	D	--
365	IM000983	CTCTCGTGTGGAGATATTAAGGTGTGA ACCACTAAGCCCTGATC	p001203	A	Scp2

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366	IM000984	GATCAAGCAGAGGGGTAAAATAAGGGCA AGCTCAGTGTTAGACAAGCTCATAAGCC AAAGCTGTGAACTCTCCAACGCCT	p001205	D	--
367	IM000985	GATCACTTCAACATCAAGAAGTTACCCA GCCCCGGGAAGAAGTACATTTCCAGGAA GCAGTGTTCATTTTTTGAGTCTGCTCC CATCCCGTTTCTCTGCAGCTGGGTAAAC TTGAAGCTGGGCTAGCCTCTGGGTAGAA GGCAGCTAATGACAACTACCTTGCCTGT CCCACGGAGCCCGGACAGAACCTGAGA TAACACACCTAGCTTGCTGAGTAAAGGC AGGTTACTGTGTGAATGACTCTGAGCTG TTCCAGCTCTGCAGAGCAGGAAGTCTGA CTGTGGAGATAAGAGATAT	p001207	D	--
368	IM000986	GTCATGATTTGTAATCCCTGTCCAACCTC TCATTGCTTAGGTCAAAATGGCTTAACTC CTAGCCTACTTCAGTGTAAGATCATGC GTAATGATC	p001209	D	--
369	IM000987	GATCAGGCTGGCCTCAAACCTCAGAAATC CACCTGCCTCTGCCTCCTGAGTGCCGG GATTAAAGGCGTGCGCCACCACTGCCTG GCTGCTTCTTTTTTCTTTTCTTTGTG TGTGTGGGGTAGTGGTGGTGGTGGTGG TGTTCAACC	p001210	A	<i>Hsc70t</i>
370	IM000988	ATGTGTGTGTGTGGCATGTGTGTGCCAT TGTGTGTGTGTGAGTGAGTGTGTGTGTG TGCTGTGTATGTTGTGGAACAGATTCTT GTGTATGTTTCCTTCTTACACATGTTTT CAGAAGTGAAACCAGGCTATGAAGACCG CCAGGCAGCTCTGCAAAGCAGTACTGAG AAGGTGGGACACTGCGGGGGTGAGAAC AGTATGCATGATC	p001212	R	--
371	IM000989	GATCACACTCCATGAAGCTTCTCTTCTGC AACAGGAAACAAATAGCAAGCAAAACCA CTGGTAATCATTATGTGGTGTCTAACAGA GAGCGGTGACAGGGGTGGAACCTGAA TGACATTTAAAGGAGCTGGAGATGTTG GTTTAAGGCGTGTGGGGGCAGCCTACA GCATGGAATTGGTCCATAA	p001213	D	--
372	IM000990	AACCATCATGGTAGCTTCTGCTTCTCTCC ACGAAGATGGTTGTTTCCACAGTTGCC TCTCTACAGAGTGGTCCTGTATTAAGTCA CAGGTGCCATCCTGGTGATC	p001214	D	--



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373	IM000991	GATCTAACCACCCGTTTCCTGCCCCGGTC TTAGATAGACCTCTTGGCCCCACGCAC CTAGACAATGGAGTAGACAAGACTTCGA GGGGAAAGAGGCTTCCCAAGATGACCC AGCTCATTGGCTTGACTCCCAACGCCAC CCACTTACACAGTGAGTATCTCTGGTCTT TGCTGT	p001215	A	<i>Farp</i>
374	IM000992	GATCTATGTCATCTTCCAGGACTCAGAG TTAAGAGAGTTACCAAGTGAGAGCTCTC ATCACCTTCTGAAGCAGTTGAGAATTGG AACCAGAAAGATGCACATGCACGGGCA CACACACACCCACGGGCACACACCCAC CCACCCATGCAGAGAGAGAGAGAGAG	p001216	D	--
375	IM000993	TAGGTTGTGCCTGGCCTGTGCAGGACAT GCCTATGGGGTCTTCATCCCTCTCACTT ACTCTAATGTTCACTACTGACAAGCACTA GTAAGAAAGTAGGTGCCTGTAAGAGACT GGAGCAGCCTGCTGCTGACTTCAGCACC TGGGAGGCCTCAGTAGCAAAGCTTAGG GTTAGCAATCCTTGGGGCTGTGGCTGGC TGAGCTCTGGGGTACCGTTTAAGAGGAA AGCTGGAGTCCAGGTTCTCCAGGCCCTG GGTGCATCCCACAACCTCTCTCTCTCTC CTTTACCACTCGCAGCCTTGGCTAAGGA TGAGGACCGGGACCTGGAGTTATCTGAG ATC	p001217	A	<i>Snn</i>
376	IM000994	GATCTCTCCCCATCCTCCTGTTGCCTCTT GTCTGTCATACCTCTACTACTCCATCAGT TTGCTGCCTCTGAGTCCCTCTTCTTCCTC TCCTATCCCTCCTCCCATCTTCCTCATCT CCAGGTCTCTCCAGGTCTTCCTTCTTCC CTCTTTTCTTCCCCTTTTCTCTTTCCACT GTCTTGATTCCCTTCCTTTCTCTGTTGG TCCCTTCCCTCGCACCTCTTTCCTCCTGT CCCTCCTTTTCATGTACCATATTTCTCTT CCTCTTTCTGTGTCTC	p001218	A	<i>Gata1</i>
377	IM000995	GATCTTAGATGGCCAAATGTTGTGAACG TTTCCTAGATGTGTCGTGAGCACTCAGG GTTGAGAGCCCTGGTTATTTAGCAAGTG AAGTGGATGTATACACAAGCAGAAGGCT GAAACTAGACCCCGGTCTCTAATCCTAT ATAAAAACCAACTCCAAATGGACAATAGA AATAAGTGAAGACTAACTCCAGGGTCA CTGGAGGGATACAAAGGGAGATGC	p001219	D	--

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378	IM000996	GAATGAATATATATATGGGACTAAATGCC ATGCCATAACCAAGAGAACTTAAAGAAG AAAGTGTTTAGTTATGCTTACTCTTTCAA AGAGTCCAGCTGCCAAAGGGATGCTGTC AGGAGTAGCTGAGAGCATACATCTGGAC CCATTAACAAAGAAGGGATGCTTCCCCA GCAAGATC	p001220	D	--
379	IM000997	GGAGGAGGGGCACCTTCTCAGAGATC	p001221	D	--
380	IM000998	GATCTTAAAGCTAATAGGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGGTC AGTGGTAAAATTGTCTACCAAGCTCTAG GTTCACCCCTCACAGAGCCGGAGAGAAA AGGAGAAATCAACTCAAGTCAACCCAAA CAAAACAAAGGACTCAACA	p001222	R	--
381	IM000999	GATCTGTTCCCAAATCCTCAGTTACTCTC TGGGAAATGGCTTCTGTATGTACACATG TTCTCTAGCTATGTAATAAAAGACCTCTC TTCCTTGGCAAACCTTAACCTACCTTAG AAACTCTGATGAGTACTAGAAAGATGA CATGTTCCACAAACGTCTTAAGTGATTCA GGGTTCAACAAAGAAGGAGATGCTAT ATTGTCTTTCATGACATAGCGTCTAAGTC CCATAGCATAACTTCTATAACACACAAGT GGGT	p001223	D	--
382	IM001000	ACACTAGCTTCGAAACTTCTTAGTTGTCT GTCCCTGAGCCCTTTGTGGTACTTCCTC CTCAGAGCCCAGCTCCAGCAGTCCCCTT AGCGGCTGTTTTAGCAACCACACCCTC TGA CTGTGGGTTTGCTCTGCAGTGGCTT TAAGGTTTGAATACGAAATGCCTTCCACA AACAGACACTACAGAATCTTAGGTGTCTG AGACAATGGGCATTTGAGAAGGAATTGG AACCTTCAGATC	p001224	D	--
383	IM001001	GATCTAAAGGGAAACCCTTGTCTTTTTGA ATCTGAGCCAGCACAATATTGTATTTCTT TCAATACGTGGTGAATGTTGTATTAGCAA CAATAAATGGAAGCAGGGAATCTCTCAT CTCATGAGTGATATTTACAATGTCTGTCT GGAAACAAACGGCTAATCAAGTTAGTCA CTTACTGTTCTTTAGAAAACACAGTACTT TGAAATGCATACCTAGCAGAGAATATAAA GTATTTACTGTTGGACTAGACTGGGCCC CCGGGTGTGAGGG	p001225	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
384	IM001002	GATCTATCTCATCCTGTTATAGCCGGAAA CATGATAGCAGGATTGGGCAACTCTCCA GTCCCTTTCTCTTGGGTAAAGTCTGAAA GCAAATCGCCCGGACCCATCTCCTGTCT CTGCAGCCTGTCCCAGTTGCCTCTGCCA CTCACTAACTTCACTCCTTAATTTAAAAA GCCAGCACATTTATTGACCGTCT	p001226	C	--
385	IM001003	GCATGTCTCCAGACTCTCAGCTGCTTCC TGTCTGCTCCTGCTGGATGCTTCATGAA GATGGAGTGAAGCAGTGGTCAGCTTGT TGTCTCAGCTGTTCTATGTGCATGTGTG CACTTGCTGGAGCTTATGTGCACCACAA GCACGCAGGTGCACACAGAAGCCAGAG ATC	p001227	D	--
386	IM001004	GATCGAACACGCTCGGACTTGCTAAACG TTTCCCACACGGACAGTCACTGCCAA	p001229	K	Nmyc
387	IM001005	GATCGTGAGTTCAAGACCAGCCTAAAAT ACACAGTGAGCCTCTGTCTTTAAGAAAC AAACAAACAACAACAGCAAAAACAAAAT ATTGCTCAAGACCCAATGTTCTCGGAC TATTTATAGGAATCAGAGTTGCTGTTCTT CTCAGGGCATGCCAGTTAATTTGAAAGA CAAGGTGTAGAGGCAAAGGAAAAGTGAT TTTACTTGGATAACCACTCATGGAGCA GTCAGGGGAACTCTAGCCTCAAAGCTCT TGCAGAAGTTATAT	p001230	D	--
388	IM001006	GTAGAAGCTTTTTAGAAATACGTTTCTTA TCTATCTATCCATCTATCCACCCATTATC ATCTATTATCTATATTTAACATCTATCTAA GTATCTGTTTATCTATCTACCTGTCTATA CCTACCTATCTACCTACCTACCTATAGCG ATC	p001233	R	--
389	IM001007	GATCGTGCATGCATGGGTGTGTTTTGGG GAGAGGTTCTGT	p001235	D	--
390	IM001008	GTTACTATTCATCTGAGGTTCTCTTTGT TGTATTTGAACAGGAGGAAGGAACCAGG AGCTCAAGGATGTAGCTGGAAATGCTAT AAAAGTGGGATGCCCTAGAGAATCACAC GGACAATCCTGCTAACCCATGGATTGTA CACTCCAATATACAAGATAACATGTTTGT GCAGGCATGCCACCATGATGTTTCGATC	p001239	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
391	IM001009	GATCGACCGCAGATGAGGTCTATGCAGG AAAAACGATGTCTGGAATTTTATTA TGCTCAGCAACTCACTGCCACGTATACT TGGAGAGCCACTTAGGGAT	p001240	K	Myc
392	IM001010	CCAAGTATACGTGGCAGTGAGTTGCTGA GCAATTTTAATAAAATTCCAGACATCGTT TTTCCTGCATAGACCTCATCTGCGGTGCG ATC	p001242	K	Myc
393	IM001011	GATCGTAGAGAGATGGACCCAAATATCA GCCAGAGAATTAGACCAGAAAATGGAAC CAAAGTACCTGTCAGTCCAAGGATGTAG TGGCACTAC	p001244	D	--
394	IM001012	GTCCCCAAATGTAAACAAAATATCAAAA GAAATTGGGCATGCCAGAATTTTGTCTT CACATTAAGGGAATTCTGAAATTGAAATC TTGCTAAGGGAAGGTGGCTTGAGAATA TTAACAGAATCCTAGGTTGAAGGAGCAG GAATAGAGGATC	p001246	D	--
395	IM001013	CAGCTAGCCCATGGAGCTGCTGGGACA CGAGGCCGCAGGCTGAGCATAATGGGG AAGAGATGGCAGATTCATTCACCCACTT GAGGAGACCACAATTAGTCAGAGGCATG CTGGGCCTGGTCAGAGTGCTCAAATAAA CATTACAGGACCAAAGTAATAAGCATT GGTGTTACAGAGATAAATCCTTTAGCAG GGACACGGGACCCAGAAAACCGGAAG GACATCGTTCCCATCATGAGAACAAGGA CAGCAAACAGTCACTGAGGGTATACTAC TGACCAGTTCCAACAGGGATGGTCAGAA GTTGAACGCTGGATATATCATGAGCTCT GACCTAAATATTCTGAGTATCCCCATGT TTGAATGGACTGAATACTCACATTTTCTA AATGCTGAATACTGAATTTTCATAGCAAC CATCATAAGGCATGGTGGCAGAATAATA TCTCTCACTCAGAAAGCAAATATTCTAA GTTGGGGATC	p001247	D	--
396	IM001014	GATCCCGTGGGGACTGAGCCTGCAGCT CAGTGGTAAAGCAGATGTCTAACGTGGT ACAGGGTCCCAGATGAGATGACACAAGT ACCTGTCACTACTCCGGGAACACTGGGT GGGACTTTTATATGTTTATTGTATTCTTA A	p001248	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
397	IM001015	AGTCCATTGTGTACTGAGAGAGGAGTTA GGTTTAGAAAGCCTTCCTCAGATGTCCC TCAAAGAAGCTGCTACAACTGCCCTCAT CCCAAGTTGCCAAGGATC	p001249	D	--
398	IM001016	AGATTGCGTGAGTTCTGATGCATGCTGG CCATGATGTGAGGCAGGGCAGTGGTT GGATTGGAGTCAGAAAACCTTCCCGTC TACTGCCGTAATTCCCAGCTAAATTCCTA TCCTCGTTGTAGCTGTTGGTGAGGATC	p001250	D	--
399	IM001017	GATCCTTCCGAATCTGCCATTTATTGAAT ATTTAAACACACCTCACTGCAGACTAAA CACATTGCAAGCACTGGGAGCAGAGGT GGCTAGTGAGCACCCTCTAGATGGTCC TTC	p001253	D	--
400	IM001018	GATCCTCCTGCGTCTACCTTCGGGTGGG ATTGCAGGCATGCACCACCATGCTTGGC TTTGTGTGGTACTGGACATTGAACCCAG AACTCTTTGAGCACTAGGCAAGCACATC CTGAACACCAGTAAAACATTTTCAAAGAG AAAAGAAAATTTAAACATACACCTATCT ACATCCATTTCCACCATGTTAGTAAACCA GGGACATTTTGAAGTGTGGTCTTTATAAA AACACCCGGGTGCTTATCTCCCACGCTC T	p001254	R	--
401	IM001019	CCAGCGGTGCTCACTACTGCATGTAACC AGCTCCAGGATC	p001255	D	--
402	IM001020	GTCTCAAAGAACAAAAATAAAAGAGGAA ATTAGTAACGAGTCCTGAGAGATAGAAG AGTATTCAGCCTGGGACCAGAGCTCTGT CTTACAGTCTTGCCATTCTGTGGGGCCT GGGACACAGCATCCTTGGTCTTTAGAAT GCCATAGGCCTCCTGAGGGAGCCTTTTC TGTAGGCACTTCTCCACATTCTTGGAT GGATGCGATTTATTCTGTGTCAGGGGAC TAGGGTGCTGGATGTGTGGGTCGAATGA CTGTTGTTCTGTCACTTGGGAATTTGGG ATAGGAGAATTCTGAGTGCAAGGCTAGT CTGCACTTGAACGTACATATCGGGTTTTA AGCCAGCCTCTGAGCTACCACAGTGAGA CTCTCTCTTAATAAAATCAACATAAATA GTCTTAGTATGGAGAGGTTAGGGGATC	p001257	C	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
403	IM001021	CGTTTTCTCGGAAAATGTGAAAAGAAG AAGCACGAGACGAAACCCCTCGAGAAT GAGAAAATTAAATCTAGAACCCAAATGG CGTCCAACAAGAACATTAGCTCTTGAAAA TGAATATTGCGCCTGCGCAGCCACCGCC CGGCCAGCTGCTCAACTGCAGCTAGAG CCCGACCCCAAGCGATC	p001260	C	--
404	IM001022	GTGTCACATGTATGAACAGCATCACATG GTATGAATGGTATCATATGGTATGACGT GAATGTGTGCACCGGCACTGATC	p001262	D	--
405	IM001023	ATACCACCCACTCCCTTAAGAAATGATC	p001263	D	--
406	IM001024	GACTGATATTAGTAGGTTGTTCTCTAAGG GCCGTGAAATTTTTAGCTAGAAAGTTCTTG CTTTCATTAACAGTGCCAAGTATGAGTTC CATCTCATGGGGTGGGTCTTGAATACAA TCAGAAGGTGGTGAGTTATCGCCATAAC ATCTGTGCCGCTATTGTACCAGTGGACA TAGTTGCCAGGCAGGCCATTACTGTAGC TCTTAGGTCATTCTGAAGCTCTCTGGG GTCTGTTAGGTGAGACTGATGATAACTC TTCTCTCCGTTAGTGTACACAGCACCTT TTAGCACTATGAAAGCGAGGCAGTATTG ATC	p001264	D	--
407	IM001025	GTTCCGATGTTTGTATCTCGTTTGAATTA TCCATCAGTTGATTAAGTTGATGGTCATC TAGGCTGATTCCCCTACATGGCCATCTC AATATTGCTTCTTTAATAAGACCTGGACA ATTAACAGCACCAAGTTGACATGCCAACTT GGATTGGGGGAGGGGTCTTAAAGGGCC CCGCCCTTAGATGAAGAGCTATACGCAA TTAATGACTGTCAGAAAGGGAGAATGGC TTTCCCAGAGATGAACCCCTAATGGAT TACCCAGTACCAAGTGATC	p001265	A	<i>Rad52</i>
408	IM001026	ATTCAACCTATGGGGCCGTTAGACCCCT GGTCTTGGGTGGGGTGGATATGTTATTC TTTTTGTCTGTGGTGGCAGCAATTTGTT TGCTTTCTTGTTTTTGATACAGTTTCTC GTCATGTATTCTGGTTGCCTGGAATTCA CTTCTATAGACCAGAATGGCCTCAAATTT ACAGTGAACCCCTGCCTCTGGCTTCAG ATTACTGGAATTACAGGTTTGTGCTATCT CACTAGTTGGTGTGTGATC	p001266	C	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
409	IM001027	GATCAAGTCCCCAGTTAAATGCTTTCTTT GATAGGTTGCCTTGGTGATGTCTCTTCAT AGTAATAGAAAAGCAACCTAAGACAAGA GGAGAGAGTGGGTTTAAGAACGAGGAG AGAGAGGAACTCAGAGGGTCTTGAGG TCCCGGGAA	p001267	C	--
410	IM001028	CTCACACATACATTCATACATACACACAC ATATATACATACACACACTTGCATACACA CAGCACACACTCACACACAGAGACACAC AGACACACAGACACACACACAGAGGAAC CCAAAGGATTGGAAGAATAATTTCCCGT GCTCAGCGGGAAAGTTTACCAGAAAGAC AAGTGGTCATGTGGGATGATC	p001270	C	--
411	IM001029	GATCATCACCAGTGTAAGTGTGGCTTTAA CGGTGCACGCCTTTAATCCTAGCACTTG GGAGGTGGAAACAGGTAGGTGTGCTTAC TTCAGTGAGTGAATTCAGGCCAGGCAG GGATACAGAGTGAGAACCTGTTATCTAA ATAAATAAATAAA	p001271	C	--
412	IM001030	CACCCACGGCTTGCTTCTTTTCTCTATGT GTAATTGAAGCACATACCCGGTGGGAGC CATGTAAAGCCTGTGTCCATGATC	p001272	D	--
413	IM001031	GATCATGTGTTAATGAAACTGTCAGGGG TTGGGTAAGATGGCTCAGTAGGTAAAGG CACTTGCCTCCTAGCCTGGAGACCTGAG GTTCCCTCCTGGGGCCACAGGGAAAAG GAGATAACCAGCTCTCTGTCCTCTGACC TCCTGGGCCCCCTCCCTCACAAACAAACA AACAAACACACACACAAACGACCAGACC ATTTCCACAGTAGCTGTGGTGCGTTAC ACTGTAACGGGCACCATGTGAGGGTTTG GGCTTTATCACATCTCCGCTAGTCATACT TGGTGTTTCTGCGTCTTGCTTACAGTTG TTCTAATGGGTGGGCGGTGATATCGAAT TGTGGTTTTAGCATGTATTTCTGTGCTC TGCTAAGACCACTTACAATTACAG	p001274	R	--
414	IM001032	CCTTAACGCTCCCTTGATGTCCACTCCC GTTTTCTCTGCAGCGATTATTGCTTAGT CTATCTATAAGGTGTATGCAAGCTGCAAA GTCAAGTATTTCTTTGTAAGTTGAGCAAG TCTCCTAAGTATTATGCTTCATAACGTTG TGATATGCTTGAGCAAATTTGAGTCTATT TCATAATTAAGCCACTGTTCTGATAAAAG ACCCTAGAGTGCTATATCTGATC	p001277	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
415	IM001033	AAAAGAGTGTTCAGATGTCAGAACTGACT AGCTGGGCTGACACTGAGGAATGAAGGT TGGGGATATATGCACCTCCTGAAAACAG GAAGCCTTTTGTGTTGATC	p001279	D	--
416	IM001034	GATCAACCTTAGTACACAGCAGAGTGTT TTCTGGGAAGCTCATGGAGACCCACTTT TGTCATCCCATAGAGGTTACTACAAATCT GAGCATGAGAATAACTACTTGCTGTTTAA TACAAAGAACCATTAGCAGTCAATGCCC CAAGTTCTAAGGGCACAGACTTCATACG AGAAAAAAAAACAAAGCAAAACAAAACT ATCACATGCTACTATCTGTACTGGGAAT GCATACAATTTGTAGGTAT	p001281	D	--
417	IM001035	GATCAGTAGAGAGCAGAGGGGTCTATGA GGGAGGTAGAGCAGCCTGGGAGGCCTG AGGAAGGAGGGACAAGGGCAGAGTCTT GGTCACTCTTTGGTCTAATTGCCTTCAGA AGGCTTGCAGACTCTGGTTTGGAGTTCC AGGTGGGTGGCTG	p001282	C	--
418	IM001036	CAAGTAGGGTTTGTGTGTGTGTGTGTGT GTGTAGCCAGTGTCTTTCTCAATCACTCT CCACCTTAATATTTTTTTTGGAGACAGAA TCTCTCACTGAACCTGTATGCTGTCAATT TGTCATGGCTGACTGGCCAAGGAGCCC GAAGAATTTATCTCTATGCTCAATCCAAC CCCCAGATC	p001285	R	--



SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
419	IM001037	GATCACATGGACCGATTGCCGCGGGAC ATCGCACAGGAGCGTATGCACCACGATA TCGTGCGGCTTTTGGATGAGTACAACCT GGTGCGCAGCCACAGCTGCATGGCAC TGCCCTGGGTGGCACACCCACTCTGTCT CCCACACTCTGCTCGCCCAATGGCTACC TGGGCAATCTCAAGTCCGCCACACAGGG CAAGAAGGCCCGCAAGCCCAGCACCAA AGGGCTGGCTTGTGGTAGCAAGGAAGC TAAGGACCTCAAGGCACGGAGGAAGAA GTCCCAGGATGGCAAGGGCTGCCTGTT GGACAGCTCGAGCATGCTGTCGCCTGT GGACTCCCTCGAGTCACCCCATGGCTAC TTGTCAGATGTGGCCTCGCCACCCCTCC TCCCCTCCCCATTCCAGCAGTCTCCATC CATGCCTCTCAGCCACCTGCCTGGTATG CCTGACACTCACCTGGGCATCAGCCACT TGAATGTGGCAGCCAAGCCTGAGATGGC AGCACTGGCTGGAGGTAGCCGGTTGGC CTTTGAGCCACCCCCGCCACGCCTCTCC CACCTGCCTGTAGCCTCCAGTGCCAGCA CAGTGCTGAGTACCAATGGC	p001289	K	<i>Notch1</i>
420	IM001038	GATCTAACTCAGGCTGTTCACTTGGCC AACAAGCTCAAATATCCATTCCGCTGTCA CATCGGGCCCCATGTGATGCTTTATATA CTAAATAGAACAAGCAAATTGATACTAGA TGGGACAGTCTGCTTACCCAGTTTGGTG TTTGGTGGGGGAGGTGAGACATATCCCA CAGTCCCAGAGCAACTGTCACTGCAGGG TCCCAGGGGAGGAGCCAGGTGTGAAGC TGGCAGTGTGTGAGGTACCCTGGGGAA AATGAATGGTTACT	p001292	D	--
421	IM001039	AGGCCTGGTAGTGACCAGCAAGTACTGA ACGCTCGCTCTATGCCAGACACAGACCC TCTTCTTCCTTCGTCTTATCCTATTATCCA TACTGAACAGACAAGGAAATGAAGGCTT AGATGAGTCACCCGACTTGCTGAGATC	p001293	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
422	IM001040	AGTGGGGCCTGAAAATCACATCTGGGCA AACCCTGAGGCCTGCCAAGTCCTCATCA GAGGGATGCCCTCTTCATCCCAGGTGCT TTCTGACTATAAAATAAGGTGAATACTAC CTCCCCTGAGGTTACACCTCCAGGGTTA AGCTGGTTAGAGAACCCAGGGACACACT GGGAAACAGCCCACAACAGCAGGAGCT GGAGCACTCACCCACGGATGTCCATGG GGTCCAGCTCCCTGCGCTGGCGCCAC CACTGGTACCAGGAAGCAGTGAAGAGGT GGCCCAACCCACTGTAGAGCGCTTGATT GGGTGCTTGCGCAGCTCTTCCTCGTGGC CATAGTACGGGAAGATC	p001297	K	<i>Notch1</i>
423	IM001041	AGTGGAACCAGATTCTCCTACGCTTTG CACTCCACTTTTCGTTTTCTCTTGTACC ATTCTAATGGAGGCCAGAGTAGCAACTG TATAGACAAATCAAATCGTTTACTCTTCC AGTCTTGCCCCTTAACAGTCTTTCCTTTG TTCTTCCTCTTAGCCTCATTTTCTCCTTC TCAGATC	p001298	B	AI604147
424	IM001042	GATCTTCTGCTTCATCTGAGTAGGCTTAG ACTGGTTTGTATTATTATTATTACTTG TTGTTGTTGTTATTTTGGTGGGAGTAGTA GTAGCAGTAGGTGTGTGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGTGTGT ATGTATATGGAGGCCAGAGAACAGCTTC TAGCGGTTGCTTCTCTCCTTCCTTCCACT GTGGTCCAGGGAATAGAACTCAGGTCAT CAGGCTGGGCAGCTGTCACCTTTAATGC TCTGAGTTATCTCACCAACGTTAATAAAA GGCTTTTCAAACAGCAGTTTGGGCTGGG CCTGGTTGTGCAGACCTGGAATTGCAGC TTCTTAGGATGCTGAGGCAGGAGGACTG GAAGCTCAAGTTGTGTCGGGGAACTTA GTAAGTCCCTATTCTCGTCCCGCACGCC CCCAAAAAGCCAAGACCAAGACCAAGCA GTTTGGTACAGCAGAAAAAGCACGAGAG TCTCCTCCTCCTCCTGCTCCTCTTAATG ATGCAGAACCC	p001300	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
425	IM001043	GATCTGTGCATTATTCTGTTGGAAATGTG ACAAGATTCTGTTGAGAAATCTCATACTCT ATGAACTCTTAAAAAAAAAAGGTTTCTGC TGTTTTGAGACAAAATTACTTATAAAGGT TTATGATGTAGTTAAGGCCCTGAATGTCC CCCAAAGACATGTGTGTTGAGGGTTTGG TCTCCACTCCGTGGTCTTTTGGGAGGTG TTTTATGTTAGCTGGTGAGGCATAGTGG CAGGGGAGGAGAGTTGGGTCATAGTCC TTTTGAAGAGGCTATTCAGGCTCTGGTG CCTAA	p001303	D	--
426	IM001044	GATCTGACTGTGATAGGAGGGTCCTGGG GCCACCCTGACATAGGCCTGGTCTATGA ATGCTCTCATGGACTGGGCCTGTTTGTG A	p001305	D	--
427	IM001045	CTGCCTCTCTCCCTGGTCCCTCTCTGAG GTTCTGGACCCTCAAAAGGCCCTTTCCC ACCCCAGCCTTCAGGCCTGTAACCCAGC CTCGGTTTCTCTCCCATGCCAAAGCAC AATGGCTGTTATAATTAACGGATTATCTC AGCGCGACAGCTGCGCCCTTTGAAAAT TAGGTTGAATAACAAGATC	p001306	C	--
428	IM001046	GATCTTGGACCACCACGTCAAGCCTCTT GTACATTTCTTTGAAAAACAAAGCTTGGT TCCCCCTAGTCACCACGGTGAAAAAAC CCAGGACAGTAAAGGTCCCAA	p001307	D	--
429	IM001047	TTAGTACCTCTGGTGGAATCACCATGCC TGACCTAAAGCTTTACTACAGAGCAATTG TGATAAAAAGTGCATGGTACTGGTATAGT GACAGACAAGTAGACCAATGGAATAGAA TTGAAGACCCAGAAATGAACCCACATAC CTATGGTCATCGATC	p001308	R	--
430	IM001048	GATCGCACCGATTGCCAGTATAGTACCT AGAGTGTCAAGTTGGCCTCTCAGGGAAG AGAGAACATGTATTAGGGTAAGACGCAA GCCCCAGTAAAAACATGTGAG	p001311	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
431	IM001049	GATCGCTTCACCAAGTGTGAACTGTTGG TAGGGACAGAGCAGACCACAAGCCCCT CTTTGCATTTACATGGGGGCGTCCTAGT GTAGGTGGCTAGGGATGGTGGACAGGA GAGGAGGGAAGACAGTATCACATAAGAA CAATAGTGGAGGGCAGGGGAGGAAGCC TTCTCATGGCTGGGGTGAAGTCACTTCC GTAGCCAGAGCTGACTGAGAATATCACT GCTTTCCTAGTAAGGAAACACCGGAAGT CGGAAGATGATAAACGCGAAACTCACTA CATCATAGACACCATTTCTGTCTTCATCAA CAGAGAAATTTATAA	p001313	D	--
432	IM001050	GATCGTCCACTTCTGTGTTTGCTAGGCC CCGGCATAGTCTCACAGGAGAGAGCTAT ATCTGGGTCCCTTTCAGCAAAATCTTGCTA GTGTATGCAATGGTG	p001316	R	--
433	IM001051	AGGGTACAGCGAAGCTTGAAAAAGCAA GGAGTGCTCTGGGACCGGGAGTGATGG AGAAAGTCTGAAGCCCCTTGCACACCC CTACAATGGGTTTGCGCCAAGAGAGGCG CCGGCAACTCTACGCGGCGTGGGGCTC TCCCCAGCGCTCTAGGTTCTACTGTGCT GAGCCACACTAGTTTCTCTCCCTAGACC TGAAGAGACCCCAGAAGTCTGAGAGTCC CTTTGGTTCTCCATCTCTCACCACCCCC CACTCTCGTGCTTTAACTCTGAGGAGGG CCACTCAAGTTCATTATAAGAACAAGG GCTTTGCTCTTAAAGGAGCCGCATACCG AAAGCGTTTGTGTGACTGAGGGTTCACA TGCACAGAGCTCCGCGTGTCTCGACATC CTCTCTCTCCGATC	p001317	D	--
434	IM001052	ATCTCAGGAACTCCTAGCAGCTTTAGTA CGCATCGTGCTGTTTCCAGCTGTCGGTA TTTTACACAGGTTTTGAGCGATC	p001318	D	--
435	IM001053	CCTTCAGGATTACTTTGGATGATTCATTA GAGAATCTTGCTTTAGACTATAAAGCAC TTGTTGAACAAGGTTACAATGTAGCAAG CAACCTTGTTTTGGAATGTATTTGCTAC ATTGTGCTCTTCCCTGGTCTGGTGCTTTC ATTTACATATTTTGCTCTTAATAGAAGTA GGGTTCAAGTCTGGGGATTTCAATTTGCT GTTTTCTCCATTGACCTCTTGAGCTGAAG TTATTCTTATTAGAAAGTCAGGGTAGGCG ATC	p001319	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
436	IM001054	CCAGCAGGCAGCGAGACGCATTTTCGC GTGGCGGTGGTGAGCTCTCGTTTCGAG GGGATGAGCCCCTTGCAACGGCACCGG TTGGTCCACGAGGCACTGTGGAGGAG CTGGCTGGACCGGTACATGCCCTGGCC ATCCAGGCGAAGACCCCGCCAGTGG AGAGAAAACCCACAGTTGGACATTAGTC CCCCCTGCCTAGGTGGGAGCAAGAAAA CTCGAGGGACCTCTTAATAAATACCTGG ATTGGGAGAACGATC	p001321	B	Mm.1045 31
437	IM001055	GTTTTTCCTGCATAGACCTCATCTGCGGT CGATC	p001322	K	Myc
438	IM001056	AAACTAGGAAAGGGTATAGCATTTGAAAT GTAAATAAAGAAAATATCTAATTTAAAAA CAAAAAAGAAAGACAAAGGAAAATTTAAAA AAAAAAAAAAAAAGAAACAAAAGCCACTG CAGGACTGCCCAACAGTCTACTGAAAC TGTGAGCCTTATTCCTAGATGAGCCTCT GATGCCTCCACTTACAAGCTACCTTCACT CCTCCATCTATCTCCTTTTGTATGTCCC GCGATC	p001324	R	--
439	IM001057	GATCGGACTCGAAGAGCAGAAGAAACAA AACTCAAAGCAGGGATTAGGTCAAATT AAAAAGGGTTTGACACAAAAGGAAACC ATCCGAAGAGACAACCTACAAAGTGAGA GAAACTTGTTTTGAAC	p001325	D	--
440	IM001058	GTCTGAGAAATTGTCTTTAATGTAGTGAC TGTGGAGCCTTGACAGGGATACCCACGAT GGGGGTGTCAATTCATATGTCACTGCACC TGGAAGACCGATC	p001326	D	--
441	IM001059	GATCGCACAGCCTGCTTTCTCAACAGTA GGTAGGACCAACAGCCTAGGTGGCACC ACCCACAGTGAGCTGGGCCTTCCACATC AATCATCAATCAAGAAAAATAGCACAAAA CCCTTTCCCGAAGGCCAATCTGCTGGAG GCATTTTCTCAGTTGAGATTCCCTCTTCC CAAATGACTGCATAAACTTGTGTCAATGT TGACATGAAACTAGCCAGCACAGGGTGT	p001327	K	Pvt1
442	IM001060	GATCGGGTAATTTAGTAATAGTTCATGAT ATTCATTACTCGGCGTAAATCAGGAAAAA CATTCTAGATGAATGTGGTATTCTCAGT GCACAGTTTGTTAGTTTAGAAAACAAAT	p001328	D	--
443	IM001061	GATCGAGGAGGGGAAGTCCTTCCTTCCT TCCTTCCTTCCTTC	p001329	R	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
444	IM001062	GATCGGGGGTTCAAGGTCCTCCTCGGG GTACCTATTAGGAGGGCAGCCAGGCTA CGTGAGACTCTGTCTCAATAAAAAATAAA ATAAAAAGCTGGGTGGTGGTGGCGCAC GC	p001330	R	--
445	IM001063	GATCGACCTGCCTCTGTCTTAAGCAAGA AGGGAGATAGATATGCATAGTATTTAGT GTAATGAAAGTTACGTTGTATTACGCTGA GGTTTATCACA	p001331	D	--
446	IM001064	ATCTAAGTAGTATAATGTTTAAGACGATC	p001332	D	--
447	IM001065	GATCGTCGTCTAACTTAGCTGGCTTTATA GTGATATAACAAAATATTAGAGGATGCTT TGGTTGAAAAAGAAGTTTATTTGCATCAC AGTTC	p001333	D	--
448	IM001066	GATCGAACACGCTCGGACTTGCTAAACG TTTCC	p001334	K	<i>Nmyc</i>
449	IM001067	GATCGTCATCATTTTTATAACAGTAGTGA GGAGATGTCCCCTGGGGCCGCCCTGGC TCTGGAGAGGGAAGCCACATGCTCCAAG GGGCTATGGTGAGGACCACAGCCTTTAC ATTTGGCTT	p001338	D	--
450	IM001068	GATCATGCACTGTCTGGGATAGTGATGG GCTGTGTCCTTTGTTGGCCAAGAGGAAG TGGCAAAGGCAAAGTTGCTGTTGGCTC CAGGAGTCAGTCTGGGGACGGGGCTGA GATGCTGTGGGACAGACTCTGGAAAGG GCAG	p001339	D	--
451	IM001069	GATCGTGGCCACTGAGAGACCTTCTTCT GGCCACCAGATGCACACAGCTGCATGAA CATCTGCATACACATTTAACACATACAAA GTTGAAGAGAAGCACGTGTGTCTTGTGG TCTGACCACTTCTGGGCACCACCAAGC TGCTCTGACAACGGATTCCCACTGGGT CGGCCATCTTGCTTCTCCCTCAGAGT TTGCCCATGTCTCTGTCTTTTCATAGCC ACAGCCTTGCCCAAGATAAGATACATCC AACTGTACAGTGCTCCAT	p001341	D	--
452	IM001070	GATCGTACCAGGAGCTCCAAGCGTACCC CTGATGCTACAACCTCATTCTGAGCCTT GATTCTGTGGACTCTAG	p001342	C	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
453	IM001071	GAACAAGGAAGGAAATAAGAATAAAGG ACATCTGACACTACCAAAGTTAGGTCAG GATGTGTCTTACAGATGGCCACTCAACA GCCTATAGAAAAGCACCGCACAGACCAGC ACGGTCTTTTTCTCCCAGGTGTCTCTGA GGTACTGCTTTCTTTCCAGGGATC	p001344	D	--
454	IM001072	GATCCCGAGTCCTTTCATCCTGTGGTTC TATTGTCCCCTAGGGCTTCAGCAGGCAG AAGGAGAAAAGACACTGTAGAGCAGCCCC CAAA	p001345	D	--
455	IM001073	GATCCTGGGATTTTCTGGGCAATTGGAG GCCACAATTTAGATAGTTTCCGGAATCG ATGTCCCTTAAAGACCAGCGCCTGGACT CTACTGAGTAAACTCCCATTCAACTTCC TCCTCTTCTCTATTTGAACAACGTGTAT CATTAAATTATAAAATTGTTGTTGTTGTTG TTGTTGTTTCAAAAATTAACTTTATTGGG GGAGGGGCAGTTGCCCGAGGACAACCTT GTGAGAACCAGGTTTTGCCTTCCACACT TAGGGGTCCTGGAATGGAACCTTATGT	p001346	R	--
456	IM001074	AGAGGAGAAATGGGGGTGCGAGAGGAC AAAGTCTGTGCCCCACAGCGCTGGGGC CAGAGCCCAGGAGGGCCTCATGGGAGA GGTTGCCTGAAGGCAGTAAGAGAGGCCA GAGGATGCTTGGGCCAGAGAGGTTCCC CACAATTGCTTGGATC	p001348	D	--
457	IM001075	GATCCCAAACAACTGGAACAGGGGTTAT CCCAAAGCTGTTGCCTG	p001349	D	--
458	IM001076	GATCCAACCTCCTCTTCACAAAGAGACTAT GTGCAGGATGGAGAAGAAGATGTATCCA AGCATATCCTGTGAAATTTATGTCAATGC TGTGAAATTTGTCCAGCACTCACAATCC AGATTTCTGCTTTTTAGGTGGCTTTTTCT ATTTCAATTTCTTCTGGCTTCATAGAAGTT TGAGGTGACATTTTAAAGACCTGTGCCA CTAAATTTAGACCCTATTTG	p001350	B	Mm.1238 02
459	IM001077	GATCGGTTAGTTTGACCAGCCATACTATA ACTTTAGTGCAACCCTTTACTTGGTGGGT GGTACTAGGAATTAACCCAGGACCTTC ACATATACTACTATCATTGAGTTACATTT CTAGCCCTTTTAACCAATTTCCCTTTAAC CCTTTTTATCCTTTG	p001351	D	--

SEQ ID NO:	MUTATION	SEQUENCE	CLONE	CLASS.	GENE
460	IM001078	CTCAAGATTCTGTTGTCTGAGAATCTCTC CCTCTGCTTGGGGACCCATTATAATGA GGTGATACTTCATCTGAAGTAATGGCCA GGCCACGGTGTGAGACTCTTGAATGTCA CATGCTGGATC	p001352	D	--



TABLE 2

SAGRES #	SEQUENCE	SEQ ID #	CLASS.	GENE
IM000127	CATGTGAGACTTGTTAATTTAGATTT ATTCTGTAGTGTTTTGATATGAGTAT AAATAAGACAATTAAATTCTATATTAG AAAGTGGCTTTTTACATTGAATATGC TTTCAGGATATGCGTGAGAATTTGGC GATGTGTAATC	461	D	--
IM000128	CCTTACTGCAGAGATGACTCGGCCA ACGGCTNCGAGCTCCTGACCACTTC CTCAGGTTTGGTTTTGTTAGTTTTTC TCACAGCAATGGGAAGCATAATCAAT ACAACCTCCAGAAATGCGACCTGTG ACAAGACCAATGAGCAGACTCAAGG CTGGGCACATAAAAGCACCAAAAAA AAAAAAAATTCCCTTGCAATTATTGT TCATG	462	D	--
IM000129	GCTGCTCATCACCAAAGGAAGTCAG GACTGGAAGTCAAGCAGGTCAGGAA GCAGGAGTTGATGCAGAGGCCATG	463	R	--
IM000130	CATGGCAAGATGGAGACTTTGTCTA CCAGGGCCACTCCAAGCACCCAGCT G	464	K	<i>Fgf3/Fgf4</i>
IM000131	GTGAAAGGGCAGAAATAATTCCTGA AGGTTGTCCTCTGCCTTCTACATG	465	C	--
IM000132	CATGACTATGTTTCTTTTAGGTATATC TGAATAGTATGGATCTAAATGATGAA GTTACACCATTTTCTACAAATGGGCA CAGAACACAGGGCATAGATACAAAT GGCAAGGTGAACCCAGATCTCTGTG CTTATCTGCAATATAACAACACTAAG AAATATTAGGTCTCTCTGTGGTTTTTC CTTAAATCTA	466	D	--
IM000133	GTATTTCTGTGTCAGAGGAAAAGAGTT TTCAAAAACTTTTAAAATTTTATTT GTTAGCCTGGACCAGTTTCATAGCAA CCTGTCATCCATATCCTCAGATTAC TTATGAGTTTGTCTGCCCATTAAGAT CTTTAAATGGTTCTAACAGCTTACT TCATTGTTCAATTAGTAAAGGGTTTAT ATCTACACTTTGATATTTGCTTACTCC ATACATG	467	D	--
IM000134	CATGAGATGAAAAAGAACCTTTTGGA CTTGAATTTTGTTGCTTCAAATGCGT	468	D	--

	ACTGCAGTTGATGGAAATT			
IM000135	AGGGTCCCTTCAACTTCCTCAGAGC CAAGGCTGACTTACTACCGTTCCCC AAGATCTCATG	469	D	--
IM000136	CATGCCTCTGGAAAGTACCTTAAACA TAGAATCCCCTCCCTAGTG	470	K	<i>Myb</i>
IM000137	CCAGATCCCATTAACAGATGGTTGTG AGTCACCATG	471	K	<i>Wnt1</i>
IM000138	CATGACTTCTTTCATTTCTTCTGTGT GTCTGTCTTCCTGTGTTTGCCTGCC CTCTCTTCTCTTCTAACAGCCCCCT TGAACCAACTGATGCGCTGTCTTCG GAAATACCAATCCCGGACTCCCAGC CCCCTCCTCCATTCTGTCCCCAGT	472	K	<i>Braf</i>
IM000139	CATGGGAATGTAATGTATTAATGAAT ATTATATAAAAGAGGCTAAATAGCTT GGCTTTAATTTCTCACTTTGCCTACT CAATTGAGAAGTTTATGGATCACCAA AAGT	473	D	--
IM000140	CATGTCCTTATTCTAGGAAGCCCCCT TTTTTACCCCTGCCTCTGAGAGAAAC AG	474	D	--
IM000141	CATGAACACCCAAATCCATATGAATA CACACATAAAATATTTATTTTCTCTA TAATTTATGCCACC	475	D	--
IM000142	GAAAGCATTGAAATATACTGGCCTTA TTAATGGCACATG	476	D	--
IM000143	CATGTGCACACACCCCAACAAATGAC CTCAGATGTCAGTGGTACTGAAACT GAGAACTGATGATAGAGCCAGTAA AAATACTGAAAGTGCCTGTTTTGAGA GTTTATATTTTACAATACTTTAATATC TAACTACACACACATACACCTGAAAA GGGCTCAGAATACACAGGCCTGAGA TGGCTCTCAAGAACCAGCCTC	477	D	--
IM000144	GGCCTTCCACTGCTCAAAGCTCAGA CTGCAGAAAAGGTTGATAGCCTCCC AGGGGCAATGACACCCTTTCTGCTT GAGCTTCCCCCCCCCCCCCTCTCAGG ATGTAGTCATG	478	K	<i>Wnt1</i>
IM000145	CATGCCAGTCCACATCTGCTTCTATG ACAAATGCCACATCCCAACGACAAA CTCACTCATTCTTCCTGTATCAATTTA CGCATACACATAATACTTTTGCTCAA GGTACATTCATATTTCCGGCAAACAG ACAGCTATAG	479	D	--

IM000146	CATGTCACTCACTTGGAGAAAGAGTT CTAATTATTTATCACGGCATTTCAC AACTATAGAAATAAAGTTAATTTCTTT GGAAATAAAGTTGAAGTTGTAATTC CAGATGGGCTCAGGTTGCTGTT	480	B	Mm.605 52
IM000147	CTCCTCCTAAAAGAAAAAAGGAAAAG AAAAGTTAAACCTGCAACAGCATCAG CAGAGCTCACCCCTCCTCACCTGCA GCCCTGGTTGCCTCTCTTCCTTTTCAT G	481	D	--
IM000148	GAAAACACTGTTCTGGGTTTCAGGGG TTACTTAGCCTTGGAATCAGAGTCTA CCCAGAGTCTACCTGCTTCTACCCAA AGCAGGTGGAAGAAGCTGCCCAGGA CGGGGCTCAGAGTCTACATTTGAAC TCCCTGTGCCAAGAAGTCTGGATAG AGTATAGTGTCTGTATATTCTAACTT TCTGGAACAACCCCTGCTTACAATAC TCTTTCCAACCTCTCAGGCCATG	482	D	--
IM000149	ACCTCTGTGCCAGCTTCTCGGACATT TAACAACCTCTGGATCATG	483	K	<i>Fgf3/Fg f4</i>
IM000150	CTGGCAGTAACACACTTAACTGCTA GCACCTGGGAAGTGGAAATAAGATC AGGAGCTCAATCAAGGTCATCCTCA GCTAAACAAGACCCCCCCCCAAAAA AAAGAAGAAGATGGCCTAGAAAGAG AACTCAGCAGCTGCTGATCTTACAGA TGACTAGAGTTTGGTTACCAGCACC CACATG	484	D	--
IM000151	CATGCCTGGTCCCTGCTGAGTGCAG AAGAGGGTGTGAGATTCTTGGAAC TGGAGTTATATACAGTCGTGTGTCAC TGTGGGTGCTGGGAACTGAACCTGT GTCCTCTGCAAAAACAAGAGGTCTT GGTTGTTGTTGTTTTGTTTGAACAG GGTTTCTCTATGTGGCCCTG	485	C	--
IM000152	GCAGGAGCCCTTGTGCAGGCCACAA CCTGCACAGCTGTACAAGGCCTGCC TGAATGCCTGAACAGATGTGTGGGA TCTTGCCCCCTTGTGCAGGCGTAC AGATGCAGACTGCTCAGAGACACAC ATG	486	K	<i>Fgf3/Fg f4</i>
IM000153	CATGGGCTAGACCTACACTGAGTTG TGCTAAAGAAGTGAC	487	D	--
IM000154	CATGTCCTCCACAGCTGAGCACCCCT CAACTGTCTCCCAGGGCCTCTGTTT TATCCAGGGTCTGCAGGGTCTCTGC CCCACGCCTAGCCCCTGAGAAATCT	488	K	<i>Fgf3/Fg f4</i>

	TAAGCAGTCTGAAAACCTACGCCACT GAACTGCTAAAACCCTGGAGTCACT GATGGAA			
IM000155	TAGTGCTAGACTCTGCCTTTTCACCT GGCATAGATTACCTTTTTCCAGATA TCCAGGGCACTTGCAAAGAAGCCAG GCATCATCAGGGGTTTGGACTTCCA GCCAGAGTCTGAGTTGTCATTGAAT GTGCTGCATTTTGTGGATTGAGCCC CAGTCTCCCGACTCTTTGTGAGTTTA GGATAATAATCACAACAGCACCCCTT CTTATTTGATGGCTAATAAGCTCTAG GCCAGTGTCTTAGCTCCATTCATG	489	D	--
IM000156	CATGTATTCTGAGAGTAGAATTTATA CCCAGAGAATACCTAAGAAGTGAAC TGACGCCGGGCGTGGTGCCGCACG CCTTTAATCCCAGCAGTTGGGAGGC AGAGGCAGGTGAATTTCTGAGTTTG AGGCCAGCCTGGTCTACAAAGTGAG TTCCAGGACAGCCAGG	490	D	--
IM000157	GCCTGGTGTGGTAGCTCACACCTTT AATCCCAGCACTCATCTCTGTGATTT GCTAGGCCAGCCTGGTATACACAGT GAGTTACACATCAGCCATG	491	K	<i>Fgf3/Fg f4</i>
IM000158	CGACATCCAAGTCTGGAAGGAGAG ATGGGAAGGGGCATTTGGGGTGCTA GGAAGGGATGGGAGGTGTCCCTAGA GCAGTGCTCATG	492	K	<i>Wnt3</i>
IM000159	CATGAAATAATGCCTTCAGAACTGCA TTAGAAATCACAAATAGCCCTGAATG CCCTCTAGATGCTTTTCTTGAGACA ATTATGTGTTAAAGTCCTAAGGCCCT TGTGAGCCCAACCATATGGAAAGGGA GAACTAACTGAAATGGGAGTT	493	D	--
IM000160	ACTGACAAGAATAGAGAGAAGTTCA GTCATG	494	D	--
IM000161	GTGTCCTGCTCCTGTCTGGGTCAAG GTCATAAAAGATGAGCCAAGGCTGA CTTCAGTGCCCACTGGGGAGACTG ATGTCTTCACAGGAATGCTCACCTG GAAGGTGTCCTCTGGGTGCATCTGT GTCACATTCGGTATAGAAGGAAGAAT GCCAACAATACTCTAAAAATATTAGA GGCCTTGAGAGTCCTCAGTGGTATT CCACCAACATCAAAGCTGCATCGTAA TATGCCAGCCTGGTCCTCACCTTTCC TGCCCTTCCCAGGAAAACATCAGCC TTTAACCTCAGCCCATAGGGGACAT G	495	D	--

IM000162	AGGATCTTATAAAAATAACAGTGACC CAAAACATAATTTTTGCCATCAAGAA TCTCAAAATCAAGTCTCATCCAAGTC TACTCTTCTTTATTGTATCTTAAACAC ACACACACGCACACATCACACAAGC ACACACACAAGAATTCACACACATAC ATG	496	K	<i>Wnt1</i>
IM000163	CATGGTATTCTGATGATAGTACCAAC ATACTGCTGCAGCTAGCTGTATCTG GAAATCCCAACCTCAGCCAAGTATTT GTGGTTGAAATAACCTATACTTCTCA CATCAAACAC	497	D	--
IM000164	ACTGTGACCTGAGCACTTCTTGTCTT ATCAATAGCTCACGTGCCCAGGCCG GGTGACCAGTCTCTAGGATGTTCTC CATG	498	K	<i>Fgf3/Fg f4</i>
IM000165	CATGCACACAAACTGGCCCTGAACT TTTGACTTCCAGGCCTCTGCCTCTCT GCGCGCACACACACACTCGCACTCC TGTATATGAAGCGTATATGTGTTTCT CTGGGAACTGTTTTATCAGGTGAAG CACTTCCTTTGTTCTTGCTACCCACC TCCAGGGCTCCAGGATCTCCAGACA GCCAACCCTAAGACAGGCCCGAGCTT CCTCTGTATCTCTGTGATGAGAACCT TGGCATAGAGCTGCCCTCACCCCTCG GGATAGGGCTTATGTTCCCCGGAAC GAGCCAGGCACCTCAACAGCTCCTG GGGAGGAATAGGGGACT	499	K	<i>Fgf3/Fg f4</i>
IM000166	CATGGCACTATGAAGGAAATGAAGA TACAAAAGATTTCCCATACAAAGGGT CAACTGTTCAATTTGGCATTATT	500	D	--
IM000167	CATGATAGAAGACCACGTCTGGGAT GGGGTAAGGGTTTCTCAGAGTACCT TGCCCTGGGGCCACATCCTAAATCT ACAACAAAGCT	501	D	--
IM000168	CATGCAAAAGAATTCCAAATGATTTT ACAGATCTTAGCCCTCTAAGAGATAG ATATAGCACAAAGTCCTGACTCCTGAG GTAGGTACACACTGACTTCCTTCCAC AAGCACTGCCTCAGCCCGGAGATGA AGGTCACATCAATAGAGACAAGTCA GGTTAACCGTGAGCAACCTCAAGAC AAGGAGGAGCACAGCATAGGTCGGT GGAAGTGTTTGCATAAGCCTAAGGC CTGGGCCCCAGTCACCAGCATTGCAG AGGAAAAGGAAAAACAGATAGTAGG TGCCTTGGTGTGT	502	C	--
IM000169	CATGCAGTTTACCAATCTTTTTCCAC	503	D	--

	TCTTTAAAAAGACAAAAAATATTAGAA TACTGGGCTGAGGAATGGCTCATCA GTTAAGAGCGCTGCTCTTTTGAAGG ACTCCCGTTCTGTTCCAAATGCCAC CTGGAGGCTATCCTGTAGCTAGAGG T			
IM000170	AGGAAGTGCTGAATAGAGAGGTTTG GGGAGAGCCCAACAATCTGACCTAT TTATACCCTGCCAGGCCCTGCCCAT G	504	K	S100a4
IM000171	CATGGTGCTGGAGGATCATCCATCC TGACATTCTGGGA	505	R	--
IM000172	CTTTAACCCTTTTATGGTGTGACCAG AAACCACAGATCTTACCTAGGCTTCA GACACATCACCCGAGGAAAGCTCCA TTAAATCCTCATTCATG	506	D	--
IM000173	CATGTATTCATAAGTGGATATTAGCA AGAAAGTACAGGCTAAT	507	D	--
IM000174	CCTCTGGAAGTCAAGTGCAGCTTTG CTTATTTGTTTAAGCCATCCACCATC CAGTTATTAGATCTGAATTCATCTTT AGGGTCAGCTTTGTTGTAGATTTAGG ATGTGGCCCCAGGGCAAGGTAATCT GAGAAACCCTTACCCCATCCAGAC GTGGTCTTCTATCATG	508	D	--
IM000175	GTTTTCTTTCTTTTTTTTTTAAAGAA ACAGTCTCAAGTAGCCCAGGCAGTC CCTAACTTATTATATAGCCCAGGAC AGTCTTGAATTCCTGAACCTCCCTCC TCTACCTCGTAGTCCTGAGACCGATT GCATG	509	D	--
IM000176	AGAGACCCAGAAATACCAAGGTGAT TTCCAAGTGCCTGACCTGGGAGGCA AGCATG	510	D	--
IM000177	CATGTAAGATCTTCACTTTTCCAGTG TCTGTTTGTGCTGCCTTCAAAGTGT GACCTGATGTAAAAATGTTTGCATCA GCTCAGGTGTATAGAATTGGACTGAT TCCAGGAGAGTCAAATATACAGAATA TCTAGTGTCCAAGAT	511	D	--
IM000178	CATGCTAATGGAGTTTATTCTTAGGA CTGCCTCCTGCATCCATTGATTGACT TAAATATGTGCACACT	512	D	--
IM000179	ACTAGGTGACTGTCTCAGGGTCTCA CTGTGTAGTCCTGGCCTAGAACTCT CTATGGAGACCAGCCAGACCTCACA CTCAGATCCAGATGCCTCAGCCTCC	513	R	--

	TAAGTGCTGGGATTAAAGGCCAGTC CCACCATAACCCTGCCCTGTTTCTGA CATTTGAACCCCTCCTTTAGACAGTA GGGAAACTGAGGCCCTGAGATATGA CACTTTTAGGGGCATG			
IM000180	AAACTTCAGAAAGCGGGGGCTACCA AGGAGACTCAATTAAGATCTCTCCTC GATCTTGAAACCATCCCCAGCCCTTC GCAAAGCACATTTGACGGACAGGGT TCTCTTGTCTTGGGCAACACATCCCG GCTACGCTCTGCAGGGTGAAGCTGT TAAGAACGTTCCATG	54 514	D	--
IM000181	GATAAGCCTCTACAAAGCTGGAGAG GGCAGTCCAAAGAACTTGAAAAGA TTAAAAGACAGTGCCTAAGGACACAA ACGTTTTTCCATAAAGAGCCTATGAC ATATTTTACTGCTGCTAATGAACTG ACCTTGAAGGAACAAGTGTTTAGGG TTAGCCTAACTTTGGAATTGGTGAA GGCAATGTGTCAGCTAGACAAATTA GAGAAAGAACTCAACAGATGAGTCA ATGAATTGTTCTAACTAGCTTGACT TAGGATTTTCAGCACAGGAACAAAAG CACATACTGTCCCTCTGGTTGGCAT G	515	D	--
IM000182	CATGGAAATGATAAAACCACACTC TAGAACATATTAGAGGAGTGAGTTAC CCTGAAGAACACATTCGTTGGAAAC GGATATTGTGTAA	516	R	--
IM000183	CATGCCCGGCTCTATTACTATTTCTT TCTTTCTTTTTTGTTTCAGGATCCAGT TTCCTTGATAAATTTTCTTGAATGTT GTTGTTGTTTTTCTTTTGCTGAGTTT TTCTTCAATACTGCTGCTTTTTCTCTC CAGGTTTCAGGATGAGA	517	D	--
IM000184	CATGCTGTCACTAAGCTGTGCTCTTC CAAGGAGATGAAGAGACTAGCTGGT ACCCTTGCTATGCCAGGCTTTCTTCT TGTTTATACACACCTAATG	518	D	--
IM000185	CATGATCTAATCTGAACTTGTATCCC AACCTTTATAAACAAGTGAATGTGT AATCTAACTAGTATAAGCTCTTGAA TAATAGCTGAGTGAATTGCCTTTGAT ACACGTTTCAAATTAGTAGCC	519	D	--
IM000186	GTCAACCACAGCAGTACTGTTACTTT CTGTGGGGGAGACGTCTCCCTCCT CATG	520	D	--
IM000187	GGCAGTGAGCTTGCCCACTCTGCTACAGGAC	521	D	--

	CTCGGTGACCCACTATATACAGCCCTCTTCA CTACGGCTCACAATCGGAGTTTAAGACCCAG TGAAGTAAACCCAGCAGGACCCTTTACAAAG CCAGGACATG			
IM000188	CTTGTCCAAACCAGCTTAGTCAACAG CCTCCTATCTGGGCTCCATCTTACCC TCCTCATCTAGCTGATGAATGTACCT GCCTTCTGTTCCCTTCCTCCTGGTCT GAGCTGAGCCTTCTTGGGACTGAGA GCCTTCATCCACCACAGGCAGACTA TCTTTAGATCATCATAGCCCCAGGTC TTCATTGCAGTGCAAAAGTGCAGAC CTTACATTTCCATTTTTATGCTCCCTT TGTAACGGCTCCTTACCGGACTGCA GCATAAGTGGCTGAGTATCCAATCA CAATAGAACACTTAGTTGTTTGCTTG TCTAACTCTCTCAGTTACACCATTGA GTATGTTACACAGGGCTGCTTTGTAG CTGTCACTGAGGCCACAAGGCAAGG GGACTAAGGCAGGACTCAGATGAGC CTGTTTTTACTTCCCGTTGTCCCTTT CACTTTGGGTTGAGCATG	522	D	--
IM000189	ATATAGACTCAATCAAGGTATTATTC TGGAACAAACAAGTAGTAACAAAAAT AGTGCAATTGCAAGTATGATAACACA AGGCAGCCTTTACCAGCTTTGTCTGG AAGGAAATTGTTCTTTGAAATCTGAA TTCCAGAGAAAAAGTCAAATGTAAAC TAGAAGTGTTTGCATG	523	D	--
IM000190	CATGTATGTGCGTGTGTGAGTGCAT CAACACAAGTGCATAGATGCGTGTG TGTTTGTGTGTCTGACTGTTTAAGTA GGTGGCATCTGTCCTAGTCCTGACT TTTGATAAGTCTACACGTTTGATAAG AGGATCTCTCTCACCCTCAGGTTCC TCCCCCACCTCCACCCAGTACAC AGCCATAACTATAAACTCCCCACGCA GATGAAGCCCCTCTGATCCCATTTTA GGGACATAACACCCCCCTCCCAGAC TGAGCTAATGCCTTGGACCCTCCAA AACTGATCTGAACCCTCTCTGACCCT GCCCTCCTCCAGCACAGGGCAA	524	B	BF1638 10
IM000191	CATGATTTTCAGTTTTCTTGCCATATT CCACGTCCTACAGTGGACATTTCTAA ATTTTCCACCTTTTTTCAAGTTTCGTCG CCATATTTACGTCCTAAAGTG	525	R	--
IM000192	AAGTATGTCTGCTATGAGTCAAAAGT CTTATTTTTGCATCACATG	526	D	--
IM000193	CATGCCGCAGTGGCCAGCAGCCCTG GTTCCAGCATTCTCAGAGATAACAAG	527	K	<i>Fgf3/Fg</i>



	GAGCCAGTGACCCTTTCTTCAAGCA CCAAAGAAAAGCTAACCGACCCAC AAAGACCTGAGTATGAATGGTTTCTG CAGCTAAGGCACTTCCTTTGAGGTC AGCGCAGTTCGGGGCTGAGAAAAGA GCTTGCCCTGGCTTAGAGCCTTTCT CTGGCTCACTGTCCCAGCCAGGACC CATCCATCAGCCCACAGTGGGGTGG CATAGTGCAATCCTAGAGAGATGTT AAAGGGACATATC			<i>f4</i>
IM000194	ATTCTCTGGGTTTTCTGTGGTGCTC TGGACCCCTCTCGCTCCTACAATCCT TCCTCCCCATCTTCCACTGCTCTGCC TAGTATTTGGCTGTGAGTCTCTGCAT CTGTTTCCATG	528	R	--
IM000195	CATGCCCTCTCGACCCTGGGAGCA TTCACCATCTTTATAAACTGATTCTTT CTGGGAAGATGATG	529	D	--
IM000196	CATGAAACACACTTTTAACTTTCCAC ATACTTTTTTAAAAGTGACCTTCCCAT TTTTTCGCCCTAGACCCAAATTGGA TGTTTCTGGCTCCCTCTCGTTCGTAG CTTTCCTGTGATGTAGAAACCTCTTA GAAACCACACC	530	D	--
IM000197	GTTTCCCACGGTGGAAGAGGCAAAC AAGATCCCTTGGGCCTGCCTTCTTGT GGCACTAATCTTACTCATG	531	D	--
IM000198	ATGTGGTGTTTAAATGAGAATGTGGC CCATAGGCTCATATGTTGAATACNTA TTTTCCAGTACTTGGAAGTATTTGGG GAGGACTAGAGGTGTGACTTTTTGA AGGGGGTGTATTATGTGGATGTACT AAGAACCTTTAAATCCCTCTGACCAT G	532	D	--
IM000199	GCATCATAGTTGTACCATG	533	D	--
IM000200	CATGGGTAAACAGTGGGCCCTAAAC TTGAACTAGAAAACCTAAAGATG	534	K	<i>Wnt1</i>
IM000201	CAAGTCTGTCTGTCTCCTTACTAGCC TTTTGCTGTTCTGACTCTCAAATGGT TCCTTAATTGGCCATTTGTCCCCTAA ATTAGGGGCGATTAGGATCAACACT CAAGCAATGTTCCAGATGGGGTCTG ACGTTCCCTCACTGGGGTCCCAGGGC TCCTCTGACTTGGTCACAGAAAGGT CAGCCCTCTGACCTGGCATAGATGT CTGGATGACCTCTGACCTCAGCTCA TAAACCTGACTGTGGAGATTGAGACT GGAGGGACTCAGGGCAGTGGCTCA	535	K	<i>Fgf3/Fg f4</i>

	CTGGACAGTGCCAGGGTGTGCAGTG GTAGGCAGACTTCTATGTCAGGTCC TCCTGTGCCTCCATG			
IM000202	GCACATATCTGAGCATCTCAAGAAG CTGAAGCAGCAGAATCATCCGCTCG AAGCAAGTGTAAGCCAATAAGAAGA CTCTGTCTCAGAAGAACTGAAACGA AGAGAGACAAAAACAATTCTGGGG CTGAAGAGATGGCTCAGCAATTA GCCCATTCTGCTCACTCAGAGGCC TCTGTGAGCTGTCTCCAGATGTTAA CAAGCACAGCTAACATTTGGCATG	536	R	--
IM000203	CACATTCATTAAAGAGACTTTATTA GCTCAAAGCACATATTGCACCTCACA CAATAATTGTGGGAGACTTCAACACA CCACTTTCATCAATGGACAGATCATG	537	R	--
IM000204	GGGGAGAGGCTTCAATGAGCCCCCT CACATTTGCATTTAAATAGCAGCATC AAGCGCTTCGCGTGCCACACACCAG TGGGCTCCCAGATGTCAAGCCGGAG TCAGTCAGATGGCCAGTGCCAGCT GTCCTCCCTATGTCGTGCCGGAGCA GGCAGTGACCTTAAAGAGACAGCGC TCACCGCTCCTGGAGCCCGACTCTG GGTCCCTCATG	538	D	--
IM000205	CTTGTCGGCCACCCCGCCTGCCTCA TTACCTGGCTCACTACTAACGTGAA AGCCTTACAGAAATCTCCAGGTCCTC AGCGGGAAAGGAAGTCATCTTCTTC CTCATCCTCGGAGGACAGAAGTCGG ATGGTAAGCATCTGTGCTGTGCTCCT CTAACTGTGACGCCGGGTTCCCATC ACATG	539	K	<i>Braf</i>
IM000206	ATATAGTATGACTGCCTCAAAACAA ACAACAACAACAAAACCCCAAGATAT CTAAAGGAGGAACATTCCAAAAGAC AGAAATGTCCATAGACCTTGACAAAG GAACATG	540	C	--
IM000207	GTCAAGTGGATGTTTCTCATTTTCAA TGATTTTCAGTTTTCTTGACATATTT ACGTCCTACAGTGGACATTTCTAAAT ATTCCACATTTTTCAGTTTTCTCGC CATATTTACGTCCTAAAGTGTGTAT TTCTCATTTTCCGTGATTTTCAGTTTT CTCGCCATATTCCAGGTCCTTTAGTG TGCAATTCGCATTTTTCACGTTTTTA GTGATTTTGTCAATTTTCAAGTTGTCA AGTGGATGTTTCTCATTTTCCATG	541	R	--
IM000208	CATGAAGTTAGAATAATTGGGATAAA	542	R	--

	GCTTTTATCATTATCAATTGGTTTTGA AATTATTGTATTGATATCTTGTAACCT GAATATTTATTGGTACATAAGTCTGG TTATGGTTGACTACTTTAAGTTTTAAG AGTTTTGATTCTTCCAGGTAAATGGG TGTGTAATG			
IM000209	CATGCAGCCGGGGTGGGATTTGAAG ATTATGCCTAGTGAATATTTAATATTA AACACGGTGTGATCGAATTGATAGCT GTTGAAAAGTAGAGCGAAACC	543	D	--
IM000210	GGACAGGGTCTCTCTCTTGTGTT CATTGTTTCATATATCATCGTCGCC TGCTTACAGACTGCATTGTGTTCCCC TGTCTCTGCCTCCCATCTCACTGTAG AAGTAATGGGATTACAGATAGATGCT ACTGTGTCTGAAAGTTAAATTCCTAG GCCCCATG	544	D	--
IM000211	AGTGGGAGGGAGCGCCACTCTTGGA GCTAGGCAGGAAGTGTGTTACTTCA AAAATAACAAGACAATCTCACATTC CTGAGCTGAAGACCAGATGCAGCCA GGGACAGGGTTCTGCCCTGGCCACT AGATGGGCTCTCTGGCCCTGCTAAA GCACTGCACAAAAGTGGACGAGGTG CACCAAGAGTCCCGTGTGTTGGCCCT CAGGGCAGACTAGAGAGCAGGACTT TCTCCTGGGAGCAGAAAGTGAACCT GGGTCTTCATG	545	K	<i>Fgf3/Fgf4</i>
IM000212	CATGCTCATAATTCTGCAGTGCCTTC TCATAACACAGGATAAAACACTCTAA CCTTTAACATTATACTTGAAAAGTTAT GTGGTTTTTCTCCTACCAGAGTCATAT CAAACAGTCTCCCTCTCCACTCACA AGGATCCAGTCACAATGGCCTTTTA	546	D	--
IM000213	CTGTAGGACCTGGAATATGGTGAGA AAACTGAAAATCACGGAAAATGAGAA ATACACACTTTAGGACGTGAAATATG GCGAGGAAAAGTGAAGAAAGTGAAG AATATAGAAATGTTCACTGTAGGACA TG	547	R	--
IM000214	CATGGCGAGATTCTGTGTCCAAGCT GCCTCTACTCGTGACATTCCAAGATG CCTCTGAGGTGGGAAGTGTGAAATA GGACAGAGCCCCACAGTCCCCTCTT	548	K	<i>Wnt3</i>
IM000215	CATGGGGGGGGGTACCAAGAAGGG ACTGCTGTGATTGGGATGTAAATAAA TAAATAAATAGAATAAAACAAAACCA AAAACAAACAGAAACCTAAACTCAAT AACTGCAGAAATGACTCTTGCTCTTT	549	D	--

	TCTGGTAAGGTTAGAAGCAGGTTAC AAATCTATATTAGAGATGGAGGCATT TCACACCAGCATAGGTATAGGAAGT AGATGAAATGAGGACTACACTAGAG TCTGTTTGT CACAACCAATTCTGAGT GATTTCACTGAGATAT			
IM000216	CTCTGAGAAACCTACCCCATTCTCCC TCCTTTCTCCCAT AAGCAACCACCTC CACAGCATTATCAAAAGACTGCTGAC AGATTGGTGGCTCAGCAGGGAGAGT CAGAGCTGTTTCTTAGGTCTAAGTTG TAGCTCCACAGTAGTATGTTCTCCAT G	550	D	--
IM000217	CATGGAACACTCAAAGCTGGCCAGG GCCCATT TACCAGGTATCCTTTGCCT TCTCAGCTGATGGGCATCAACACATT AATTCACATATGACTCGTTTGTGTCA TATCAATAGTAT	551	D	--
IM000218	GTGGTTTTTGTGGTAGAGAGACACA GAAGAACTGAAGTCCTTGAACATA ATTATCACTGTGGTTGAATGTTTGTG TTCCTATAACATCCTATGTAGGAACT GAACCTATAAAAGTAGTGGCTCCGA AGGTGGTGTCTTAAATGTGAACTG GGCTACAAGATTTTGCCCTTGTGAAT GGCTTTATGGAAGAGGCTGTCACTTT TCTGTCTCTTCTCCATTATCTTGA AGACACAACAGTTCAAGGTCTCATCT GGGAAACAGAGACCTTTACCAGACC CTAAATCTGCCAGTGGTGTCTTGATC CTGGTCTTTCTGTCCTTAGGAGCTAT AATGCATG	552	D	--
IM000219	GGCCACAGCCAGTCCACCTGTATGC AGCTGGGTGCTTGGAGTGGCCCTGG TAGACAAAGTCTCCATCTTGCCATG	553	K	<i>Fgf3/Fgf4</i>
IM000220	CCTTAGGGCCCAAATCCTTCCTCC CATTCTTCCATAAGAGTCCCCAATCT CCATCCACTGTTACCTGTGGGTGT GTGTATCTGTCTAAGTCAGCTGCTAG GTGGAGATGCTCAAAGGACAACATG	554	R	--
IM000221	GACAGTAAAGAAGACAAAGAAGTGA GTAGAGCTGGATGAAAAGTAGGAAG TTCAGACAAAGACTGCGGGAATGAN GTGTAGAGTCTAGAGCCCAAACAGT TAAACATG	555	D	--
IM000222	CTGCTACATTCTTAGCTCTAGCTAAC TAGCATCAATTGTCCCAACCCCTTCT ATGTATGACTCCAAAGCCAGTGTCA ATG	556	R	--

IM000223	CATGGTCTCTAGAGCTAAGAGATAC CAATGCTGCGGCAGGCAGTTTTATT ACAATCATTACAGTTTTGACAGTGTC TGGCCGTGTGCCAAGGCTGGCCTTC ATCCCTGAGCTCGGTGATGCTTCTG TCCTGGTCTTCTGGCTCGTCACAGC TTAAGAAAGTAGCTGCTTCTC	557	D	--
IM000224	CATGGAAAATGATAAAAACCACTG TAGAACATATTAGATGAGTGAGTTAC ACTGAAAAACACATTCGTTGGAAACG GGATTTGTGTATATCAATGAGTAGTT A	558	R	--
IM000225	CATGGAAAGATAATGTGTAAATTTGG GTTTGCCGTGGAAAACCTTTGTTTTCT CCATCAATGGTAATTGAGAGTTTGGC TGGGTATAGTAGCCTGGGCTGGCAT TTTTGTTCTCTTAAGGTCTGTATGAA GTCTGTCCAGGATCTTCTGACTCTCA TAATGTCTGGTGTAAGTCTGGTGTA ATTCTGACAGGCCTGCCTTTATATGT TACTTGACCTTTTTCCCTTACTGCTTT TAATATTCTA	559	R	--
IM000226	GGTAAGAGTGGGAGAAAATGGGGGT GGGGGGTGGGGACACTGCAGAAAC CTGGGAGAAAAAAATCCAATAAAA TCAGGAAACACATG	560	D	--
IM000227	CACCCCCATCCCGCAGTTCCCAGAG GGAACAGTCCCAGCAAAAATACATG	561	D	--
IM000228	CATGGAGATGCAATGAAAGCACACA ATATTGCTGAACCAAACAGAAAGCTC AAAAC TAGGCACAGAAAAGAGATAC AAACACAAATCTGAACAAATTGACCT TCTCCCTATAGCATAACTAATATCTC AGAGATAAAAGTGGTCTTTATATACC AGGGCGAAAGAGGTCTAAAAGAGA GGAATAAAAAATATGGCATATTTCT GTCATATGCAGAACCTATATGAGTCT TTTTGTTTGTCTTTCAATACAGCCT ATGTAGCTCTAGCTGTCCTAGAACTT ACTTTGTAGACCAGGCT	562	R	--
IM000229	CTGTTCTACAATGCCGTTTCCAACG TATGTGTTTTTCAGTGTAACCTACTC ATCTAATATGTTCTACAGTGTTGTTT TTATCATTTTCCATG	563	R	--
IM000230	GACAGGCTCCAATCAGATATACCAA GGGCAGGAAGCACGTGACAAAATCA GATGCCTGGAGACAAGTGTAATAAA AGAAGCAACAGAAAACAAGTTACTT GGCATTGTCACAACCCAACCTCTCCC	564	R	--

	ACCATAGCAAGTGATGGATACACCAT CACACCAGAAAAGCAAGATATGGAT CTAAAGTCACTTCTCATG			
IM000231	CATGGGTCCCTGAAGGGTCTCTCCT TTAGCAAACCCCTGTACAGTTGAAGT GANTTTTCAGGTACCCATTGGTCTTA GC	565	D	--
IM000232	CCCCACTCCTCACAGGGCTCCCCAC ATCTGCCCTGGGACACCCCACTCCT CACAGGGCTCCCCACATCTGCCCTG GCACCCCTCCATTTTTTCAGGCACCT GAAGTCCCTACTTTCTAAAGGCCATT CTTCTACCTCAGGTCTTGCTCTAGGA CTGTCAACATG	566	K	<i>Fgf3/Fg f4</i>
IM000233	CAGGACAGCCAGGGCTACACAGAGA AACCCCTGTCTCAAAAAACAACAAAC AAAAAAAAGACCATTATGCATTCCTG CGGCTCTGACATG	567	R	--
IM000234	CATGGGCAGCACCTCGTGGAACACT ATTATAAGTGTCTCCAGTCAGGTCA ACAGCGTAAGAT	568	D	--
IM000235	CCTGTACATTCTGTGTTAAGGACAGA GGGCCTCCTGCATG	569	K	<i>Fgf3/Fg f4</i>
IM000236	CATGGAGGCGCAGGAGTTATTGTCT AAAGTTGTGAAGATGAAGCCTAGATT GTATTGGAGATCCGGGTAT	570	D	--
IM000237	GCAGATATTTCCACCTCTGCCTTCCA CAGTCCTTCCTCCCATG	571	C	--
IM000238	CATACGCTTACAATGTGTTGTTATTT CTGGTTCTCGTCTGCCTTCTTTATAA AAACAAATCCACTAAGGTGGAGTAG CCAGCCTTTACTCAGGGACTGTCAC CATG	572	D	--
IM000239	TTCTGTATATATTGTGTGGTCAGAAA ACCGTGGTTTTCTGGTGTCAAGAG TTAACTTTTTCAGTAATCACTCATTCT AAACCAGACAAACCTTTAATCTTTCA TCTGGAAAGGTACTCATTCAAACCAA TGCTCTCTTAAACAGAGTATTTAA ACAGCCAACTGCATCTTCAGGGTTTC ATAGAAAATCAGCTTGATCTAAATA GTCACTGAATTCTGATATCATAGACA TG	573	D	--
IM000240	TCCACCCACCCACCCACCTGCCCAC CCAGACAAATGTTCACTGAGCATTCA TATACTCCATTCATTCTAAGTACAG AGCCTAAGAATATGAGAAAATCCTCA	574	D	--

	TAGCAAAGAAATGCCTCTTGCAACTC GAGTAAAAACTCGAGTATGGGATGG AAGAGTTGAGAAAACAGATGATAGTA TGAGAGCCTATG			
IM000241	AGGAGCCTAGCAGAATTGCCCTCTG AGAAGCTCCACCCAGCAGAAACAAA TGCAGAGACCCATCGATAAACACTG GACAGAGCACAGAGTCTTGTGGAAG AGTTGGGGGAAGAATTGAGGAACCC AAATGGGATAGGGACTCCACAAGAA GAAAAAGAGAGTCAACTAACATG	575	R	--
IM000242	CATGTCCTACAGTGGATATTTCTAAA TTTTCTCCTTTTTTCAGTTTTCTCGC CATATTTGAAGTCCNAAAGTGTGTAT TTCTCATATTCTGTGATTTTCAGTTTT CTCGCCATATTCCAGGTCTACAGT GTGC	576	R	--
IM000243	CATGTGGAGGCCAGAAGTCAACATA TAGTCTCCTTCCCAATTACTTGTCAC TGGAGAGC	557	D	--
IM000244	GTTCACTAGCCAGCAGGGGGGATAG GACCAGCCCAAATTCTCCCTTTGCTT GGCCTTGACTACTAGTCTGGAAGG GATAAGTGGGCTAACCAGAAGTCTT CCACATCTCTAAGTGATTAATAATGG AAGACGTGATCTCTGGTCATTCATAA ACAGGCATTTCTCAAAGTTGGTCTGT GCAGTTTGTGGGAAAAAATGAAATGT ACTCATG	558	D	--
IM000245	CTACAGAGTGAGGTCAAGCTCGAGG ATAGCCAGGCAGGGATGCACAGGGA AACCCTGTCTCAAAAATCAAAACCAA CCCAACAAACAAAAACAAAATGGAA GGATAGAAGAGAGATAATCCATG	579	D	--
IM000246	CATGTACTGAATCCCTGAAGTTGATG CTGAGCACCATCTTGTGCTGTTCTAC CGCATTTACTGGGG	580	D	--
IM000247	CATGTGTCACTCAAAGGCTGCTGAG AATCAGGCTGTACCTGTATTCCTAAG CCATCCACAGCCATCCTGACCCACA GCAAATGCTGGCAGTCGCCCCACAG CTGGACTCCGTTCCTCCCTCCACTC CTATAGCCGAGGCTATCCACACAGG CTATTTCAGTGCCCTAAGCCTTGCTA CCCTTATGTATACATTGAGGACAATG AT	581	D	--
IM000248	AGAAACCACTGCCAAATCAATACATT TTAATTGGAAGTGTATTATGAAGCCCA	582	C	--

	GGAGAGATCCCTAAATGTATTAATTG CTTCCTGAGGAAATATAAACTCACA GTTACTAAAGCCATG			
IM000249	ATCTTCTACACAGATGAAACTGACAA AGTACAAATAAAGATTATATACCAA ATGAAAAAAGTAAACAGCACACATT TATAGATGCATCTAGCATCCCCCAA GCTCAACACCATCCATACTTGAAGAC TGCAGTGGTCCCTCTAGACAGTATG CTCCAGGTCAGCCCTCAGCACTTGA GAATAAACAGCTTCATTTACTCAGCC TGTTGTCAGGATCCATG	583	K	<i>Fgf3/Fg f4</i>
IM000250	ACTGCCTCAAAACAAAACAACAACAA CAAAACCCCAAGATATCTAAAGGAG GAACATTCCAAAAGACAGAAATGTCC ATG	584	C	--
IM000251	CATGAGCTGTGATAGTGACCTGCAGTCAAG GAAATCTGAGGGCTTCCTAATTAACAGAGGA GCTCTAAATGAGAGTAACGCGCTCCACAAAC CCCCTCACACTCGGTAAGTGTACGGTGCAG ATAAT	585	C	--
IM000252	GCCGCGTATGTGTTTCTTTTCATAGAAGAAT TAGCACATAATGGAATGTGCGTATCTGAAGT GCACAACTGAGGAGTATTTATTATTACATACC TTTACAAGATATCTTTTCTCAGGGAGCAACCT GAAAACATAAGGAGAAAAACATAAGAACTGC CACTCTAAGGGTTGGTGAAATGGCACAGCCT GGCGGTAGGACACACACATG	586	D	--
IM000253	CATGGAGAAACCTGGGCTTATTCAAGCAGTT TCCTTTGTTTACCCTGCCAGGGTTGCCAGT GAAGGGGCTCCTCCATCACTAACTAAAGGTC TTATCCTATGCTGGTTCCTCTCCACCCACCA T	587	D	--
IM000254	TATAGGAATAGAAATTCAGAACTTATCAGTTT GTTTTGCTTCAAATGTCAACACATAATTTAAAT TTACAAACCCCTTGACATTTGCATG	588	C	--
IM000255	GAAGACAAAAGATGTGTCAAATACCTGGGCA AAAGGGGGTGGTGGTGCTCTTTCCAACTC CTGAAAGACACCTCTGCTCAGCACACTAGTT TCCAGGTTCTGGGTTAGGATTTGGGTGAGA TTGGTCGGCGATGGTTTGGTTCTCCATTCT GCTGCTTCTCCCTGATACATTGAGTTACAGCA GCCACGCGTACACACTCTCGCACATG	589	K	<i>Wnt1</i>
IM000256	GAAGAGGAAATAAGGCAATAGCTAGACTGGA AAAACGAGCCAGCCTAAGAAGCTGCAGAGTA GTCTGTGGGGTTCTGCTTTGGTTAGCTGCCT TTAGTGCTCATG	590	D	--
IM000257	CATGGATAGAGGATGGAAGTTGAAA	591	D	--



	ACCTGCTATTAAGAACATAGCCCTGT CCATTAGTGAGAGTG			
IM000258	CATGTGGCCCAGGGGCACTTGGAGCCTTAG ATAGCTGCCTTTATGGCTCCTGGTGGCCTTG GATGTGGGTGGGTGACAGGAAACAGGAAGA GCTGGATAGTGGGGGGTCCCCAGGAGGAGC TAGCTGTGCTCTCTATCACTTTTGCTCTCCTG GGGCTACCCCCGTCTCAGGGGAAGGCCTGT GACTGGCTAAGCAACAAGTGTGGGCTGAGAC CTTTCTCTGTGACACTCTGGTGTACTCTGG CCATAGCACAGATCTCTAGGAACGCACTCT	592	K	<i>Fgf3/Fg f4</i>
IM000259	TATATGGATATGTTTATGTGAGGGTAGGCACT CCTGGAGGGTGGAGGCATTAATTAGATCCTC TGCAGGTGAGCCACCTGACATG	593	D	--
IM000260	ATATGTGGACTGTAGTCATCTTGAACATCTGT AACAAAATATATAGATTAGGAGTTTAGACAG CAGACATG	594	D	--
IM000261	GTGCCTCTTGTCTGCCAAGCTGGTATTGTAG CATG	595	D	--
IM000262	ATTTGTGACATCTTAGGAGCTTAGGTTGGTCT TCGAGACACAGGGCTGTCCCCTGTAAAGCAG GTTCCATCAGTGA CTCCAGGGTTTAGCAGT TCAGTGGCGTAGTTTTCAGACTGCTTAAGATT TCTCAGGGGCTAGGCGTGGGGCAGAGACCC TGCAGACCCTGGCTAGAACAGAGGCCCTGG GAGACAGTTGAGGGTGCTCAGCTGTGGAGG ACATG	596	K	<i>Fgf3/Fg f4</i>
IM000263	CATGACGACTTGAAAAATGACGAAATCACTAA AAAACAA	597	R	
IM000264	CCTAAGTCTGACCGTGCCACTTCCCAGTCTT CCCTACACTTCAATGCTTTTAGGCACAACAAA TTTGTACCCCTCATG	598	B	Mm.102 899
IM000265	CCCCCAGCCTGCTCCCTCCCCGGAGGGAG TCCCCAGTGTGACATG	599	D	--
IM000266	GTTTAGGTGATAGGGTACTTGCCCAGCAGTA GGTGGTGCCCAGGATTCTATCCTCAAAATTG CACAAACAGAACATG	600	D	--
IM000267	CATGTTGTGTAGATACCTACATAATTATAATT CATAACTGTAATTTGCTAC	601	D	--
IM000268	CATGGGTTTGAGCCTTGTCCTGAGCTGGAGG AAGAGAGTGACCCAAAGGGACCTTGGTAGCA GCCAGGGATGTGTTGGGGAGCAGAGAACT TTTATGAACCTTCAGTTTCAGTACTGAACTTC CCTTTCCCTAGACTTCCTTTG	602	D	--
IM000269	CATGGGACAACCTCCTTTTCTTCTGGGTCA GGGGAGAGAGACCTCCTATCTAACTGTATA	603	D	--

	GGCCATTGCTGTAGCCCTTAGCTCACTTCCG GGCGGGGAGGAGGAGGTTAAGACCCTAT			
IM000270	CATGAAATGAAAGAACAGAGTAGCAATTTGG GGAGAAAAGCCTGCCGAGCGGACTTAATCTT TCCCAAGTGCTATCAGT	604	D	--
IM000271	ATGCTTGTCTTTCCCGCCCATACCTGCTTTT GTTTGAGATAATAGTTTTGTTACTTTATCAACT AGTAGCGACTAGTTTACATTTGGTTTCATAAA TAAGATCCATTTTAATCTGAGTTTTCCATCCTT GATTTATTTTGATTCATTTTAATTGTCTAGT TCCCATCCCTGGGCAGGACTTTTTGGGAAAG TCTTGCAAGTGACTATGTTGAGAATGATTTAT GTTGTATTAGCACAGGTACATTCGACAGTGC TGGTTCCTTCTGGAGCGCCTCGGGTGTGGGT CCTTTTCCTCAGC	605	D	--
IM000272	CATGAGTTTGATTATTTCTGAATTCTACCTC TCTTGGGTCTATTTTCTTCTTTTGTCTAGAG	606	R	--
IM000273	GGGATAAGACTGGATAGTAAGCCGGGCGTG GTGGTGCATG	607	D	--
IM000274	CAGAAGGTAGTGTTTCACAACAGTCCTCCCG ATGATCAATTGTTTACACTAAACCATATAGG AATTCACCCTGAGAGGAGTTCGAAAGCCTTT CAAAACCTGTA CTGATATAAAGCAAATCTCTT TTGGATTCCCAATCAAAATGATTTGGCAGAAC TTTAAGGCCACAAAAATTGTGTCTGAACAACC CCTCTGAGCCCAGTTTTGTTAGCTTAAATTA GGGCCATG	608	D	--
IM000275	CCTCAAATAAGAAGCATCCATTTGGAAGCT GCTGGGATTAAGGGAGTATGCCACCACCACC AGCTATGGCATTTTTTCTTTAATTTTACTATT TTTTTGCTTGATATTATGGTTTCCAGTTTTGT GGGTTTTATAAGCTTTGAGTGTGTTTCTGCAT G	609	D	--
IM000276	GTCCACTTTAGGACGTGGAATATGGTAAGAA AACTGAAAATCATG	610	R	--
IM000277	CATGGTCAGCTCTCACTGCCCATCCCTGT CTCCAGTTCACGCACTGTATCCTGTGTCTTTC TCTGTGGCTAGACTCTTCTTGGGGGAGGG GAGTCTTGATATCGATGTGTGCTCACGCAC ATAGAGGCTAAAGATTAATCTAGGTGATTCA TTCATCGTCTCATTGC	611	D	--
IM000278	CATGTGTTTCCTGATTTTAGTTGGATTTTTTT CTCCCAGGTTTCTGCAGTGTCCCCACCCCC AC	612	D	--
IM000279	ATGGTGTCTGTTTCATAGCAGTAAACCTTAAC TAAGACACTGATATAACTCACCTTTCCAGCC TCAAAGTCTCTACCATCTCAGGATCCACTCAC	613	R	--

	TCATTCACCAAACCTTCATCAAATGCCCACTGT GCTATCATCAGTACAGAATAAATCATG			
IM000280	CATGAGACTGTCACAAGCTCCTGGGATGGGG ACCTTACCAGAAAGCCACCAAATCAGAGGCA TCCCTGTTTGGTGAGGGTACATTTGTTTTCC CCAGGCCCTGAGTGCCAGGCAGGAGCAGGC AAAGTTCACCTGGGAGGATGCCCTGGAT	614	K	<i>Fgf3/Fg f4</i>
IM000281	GTTTTGGTTCTTTCAAAGAAAAACAAAGGTC ATTGCAGCTTTTTGTACCATTGAGGTGATGGT AGGAATTGAGATATATAATCTACTTGAAGATA TATATTATGGCATG	615	D	--
IM000282	CCGCTGCTCTCTCACCAACCCAGTGTGTCTG CTTTTAGCCAGACGGGGGAGGGGGTAAGG GGGTGGTCTGTCTCATG	616	K	<i>Wnt1</i>
IM000283	GTGTCCCTCCTGTCGTTAGGCAGTACTTCCA AATCAAACCATG	617	C	--
IM000284	AGCTGGTACAATGCTTAGAGCAGAGCTGCAG AAGCAATACAAGAGATCCTGGCTCAGCTAGG TGCAAGCTGGAATAGACTCCTGACAGTTGTC CTATGAACTCCATACACAGGCATG	618	D	--
IM000285	ATGGATCCCTGGGGGGCAGTCTCTGGATGG TCCTTCCTTCTGTCTCAGCACCAAACATTGTC TCTGTAACCTCCTCCATG	619	R	--
IM000286	CATGATGCACTTAGCAATTCCTCAATTGAGAC TCAAGTGAGCCTAGGCTGTGACAAAATGACT GTAAAACT	620	K	<i>Fgf3/Fg f4</i>
IM000287	CATGTAAAGCTAGTTCAAAACATACTAAATAA TTCAGTTGTAGAAGAGGTGAGGTTATCTCACT GCCAGGATAAGCTATTGAACAAGCAAGGGTT CTCACTTACTGTTTAAGTGGAAGTGTTTTCTT ACTTCAAAAAGTCATTAATGAATTTTAAGCTG CATAAATATTTAGTTATT	621	C	--
IM000288	TAAGCTTTTTCTTTACACAATCCCCCGGAAAC CCACAGTTTAGGTCACAAAGACCCAGGCACC TATTCCTAGGCCTGGTAAGTGGGCACCCACC ATTTACAAAGAGCTCAGCATTGGCTCACACA TG	622	D	--
IM000289	CATGAAGATGAACCGGGCTTGTCTCTGGC AACTAGGCTCAGAAAGGATAGGACCACCAGC CGAGTAGCTGTCAGATGGAGCTGAAGACCTG AGGGAAAGAATGCTTGTGGGAAGAAGCTGG CTCCTTTTGGTTTTGTTGTTGCTGGTTTTGTG ACCGGATCTTGCTGTGTGACCCTACCTAACA T	623	K	<i>Wnt1</i>
IM000290	CATGGACTTAATTTTACTGCATTTGAATTATG GAAAATATATATGAAAAGTCTTTAGAAAAAGG CAGAGGACGAAAAAACCAAAGAAGCTTAATT	624	D	--

	ATCTGAGACCAAGAAAACCTCTTTAAGAAAAAG CAGTAGATTTAACTACGTGTTGTTAAATAG TCCTGTATAGATATAAAGTCCCTCAGAGGGA AGAGATTTGTTGAATAAATTCAGAACTCAAG AGAA			
IM000291	ATTAAACAGCCCAGTGCCTCAGAAGTGAAT GTTGAGAAGTGGGTAATCTGGGGACAAACAG AGGGAAGAATAGTGCCCTTGGCACGTGCAAA GGAGTTTGGGAACAAACATG	625	K	<i>Fgf3/Fg f4</i>
IM000292	CATGTATGACAGTGAGGTCAGGAGTGCCCAG GGAGCTTGCAATTGGCAGAACAGCCTTTCTG GCCAAGCCTAGTGTCATCAAGTATATATTGGA CCAGACCTTATAAACTTGGGTTCCACTCTG GCTGGACCAGCCTCAAGGCGTCGCCTCTCC AGGCCTACCTCCCAGACGCAGAGGCAGCATT TGGAGGATTGAA	626	D	--
IM000293	CATGGGAACTTGTTCGAAGCAAGGGACTCTG CTACACCTTCAAGGGACGCTGCTAATACTGG GTTCAACCTTGGGCAGCGTGACAGCAGGA GTGGGAGGGCTCTGATGAGGAGAGCCACCC ACACTGTGAGATCTAGGAGATAAGGTCACAT CCAC	627	D	--
IM000294	CCCTCCAGCAAATTGAAATACGAAAGACTCA AACACATTAGAACCATTCCAATAAAAACTTGC ATTGCCCCAGGCCCTCCACCACCATG	628	D	--
IM000295	CAAGAGTATATATCCAAGAAAAATACAGCTGA GTTGACTGTTAGTTCTGTTTTGGCCTTCATG	629	D	--
IM000296	GGTAAAACTCTACCAGTTAACTAC ATTCCCAGCCTGCCTCCAATGAATTT AATTTGTGTTTTAGGGTTTCTGTTAT TGTTGTTTTTGAGACAGGGATTACACA AAGATCTGCCTGCCTCTGCTTCCTGA GTGCTAAATTAAGGTATGCATG	630	R	--
IM000297	GTTTAGTAAGTGTCTTCTGTATTACTTTTGTG AAAATTAGATTGTTCTGGTGACTTTGTGTGC TATATTCTCTGCATG	631	D	--
IM000298	CATGTTTCTGCTTCTACTTTATCCACCCTGCA CACACTGACTGCTATGTTCTGTACCTTTTCC ATCTCTCCATTGAATATTCACTCCAACAGTGG CATTGGAAATTGCAGTGGAGATACC	632	D	--
IM000299	ACGATGGTCTTGCCCTTTCTCACACCATCAAT AGTCACTCAGAGCTGTGGTTGTTATCTGAAG TGTGTTGCAGTCCAACCTTGCCCCATG	633	D	--
IM000300	GGAGTGTAAGCGTCGGTGTGTCACCCGTGA GATTAAGTCAAAGTGACATG	634	K	<i>Wnt1</i>
IM000301	TAGACCCAGTCTTGCACTGGCCTGG GACTCGCTTATTAGGTTTGAAGTGTGA	635	D	--

	TCTGGCCAACAAACACCAGGAAATG GGGTGACAGGTGGTTGTGAGCCCTC TGAAATGGGCATTGGGACCTGAACC TGGGTCCTCTGTAAGAGACATG			
IM000302	TCACCCAGCTGGGGCTGTGCTGAAGACTCT GAAGGGGAAGATAGGCCTATGGTNACATG	636	K	<i>Fgf3/Fg f4</i>
IM000303	GTTGGGCTGAGCCACAAGTACACCTCCACTC ACTGAGCCATCTAGCAGGTCCCAAAACAAGGT GACTTTTGTGTCATCCAGCAAGACATAGCCATCT ATGCCAGTCATCCTTGTCATG	637	K	<i>Fgf3/Fg f4</i>
IM000304	TAACATATTTGCTTGTTATGAAGGAAAATGTT GGATGTGTGTGCCTGTGGTTGAGTACTGCAA GTAGTGTGAGGGAAGAGAAACCTAGCTTGAA CAGTCCCCTCATCTCCTTCATATCCTCACTCC TTGTCAGGCCCTGTATTAGGTAGTGCTTCCC TACCTCCCTAATGCTGTGACCCTTTCTTTAAT AGAGTTCCTCATG	638	C	--
IM000305	CATGTGAGCACAGGTACCTATGGAA ACCAAAAGTGTAGGATCCCTTAGAAC TGGAATTATAGGCAGCTGTACGCTAT TGATGTGGGTGCTGGAAACTGAACT CCAGGCTTCTTGAAGAGCATCAACT GCTCTTAGCTGG	639	D	--
IM000306	CATGTAGAGACTGCCATATCCAGGGATCCAC CCCATAATCAGCATCCAAACGCTGACACCAT TGCATACACTAGCAAGATTTTATTGAAAGGAC CCAGATGTAGCTGTCTCTTGAGACTATGC CGGGGCCTAGCAAACACAGAAGTGGATGCT CACAGTCAGCAAATGGATGGATCATAGGGCT CCCAATGGAGGAGCTAGAGAAAGTAGCCAAG GAGCTAAAGGGATCTGCAACCCTATAGGTGA AACAA	640	R	--
IM000307	CATGTCCTAGAGTTGTTCCAGCACAGAAGCT TTTGGGAGAGACCACCATTACTGAAACGCAG CAGATGCTGCAGCT	641	D	--
IM000308	CTGCTTGTTGTGGGGACCAGCCAGACACCCT CCACAGGTGCAGTGGTGCAACATG	642	K	<i>Fgf3/Fg f4</i>
IM000309	CATGATGTTTGTGAGGAATAGAAACCCTGA CTAAGACAGAGGATATTCAAGATCCAACTA GCAGGTAGCTGTGGTTCC	643	R	--
IM000310	CATGAAGCACACATTACCCTGTGACTTGCTTT TTTATTAAT	644	D	--
IM000311	CATGTGTCCTCTGTCTTGAGTCTCTATTCT TTGTGATTCCGCAGCTCTCCATAGAGTGAG TTCTATGTCCTGCCTGCAAGGTCCATTGGCTT ACTAGGGTCTGCCCCTCCCAGAAGAGTAGCT CATTTAGAATGCATTACTGGTGTGCTGTCTTG	645	D	--

	CATCTTTTTTACCCAT			
IM000312	ATCTATGTTTATGCACTACTAATTACTGTTTAG TTTATATATGCCCTAATAATTACCCATTGAAA ACTTAAATTTTGTTCAAAAGTGGGTCTCATT GGAGGTGTTAATGTACAATGTCTTTCTCATG	646	D	--
IM000313	CATGGCCAGCTGAGCGGGCTGGAACCTGCC CTTCTGCTTCCTGTCCCTGCACCTCAGCACC GCTGTGCACTTGGTACTAGACCTCAATCACC GCAG	647	D	--
IM000314	CATGTGCGTCCCCCCCCAAACACGCAAGCGCA CACCCACAAAGAGAAGAGACAGGG	648	D	--
IM000315	CATGGCCACTTGGAGAGAAGGGGGAAGGGA ATGCGGAGAGAGCGGGAGCAAGAG	649	C	--
IM000316	CTTAAGCACTGATCAATGGCCAAGGTTTGCC GACTTGGGATCTGGGGTATAGACATCCACCC ACTGAGACCCTCTAACAAAACCAGATGTGGA GGTACGAAGCCTGGCTCAGGGGCCTGTCCT TTGTCATCAGAATTCACCAGCTGCAGCTCCT GGGTCAGCTTTGTTTGGCATG	650	K	<i>Fgf3/Fgf4</i>
IM000317	GTGTATTGATATGCAAATGTGTAAATATGA TTTAAATTCCCCATG	651	D	--
IM000318	GCAAAGTGTCCACACTTTGGTCTTCGTTCTTC TTGAGTTTCATG	652	R	--
IM000319	ATAGCAGGTCCTGGATACCCCAACATACCAG AAAAGCAAGATTCAGATCTAAATCACTTCTC ATG	653	C	--
IM000320	CATGTCCTGGCTTTGTAAAGGGTCCTGCTGG GTTTACTTCACTGGGTCTTAACTCCGATTGT GAGCCGTAGTGAAGAGGGCTGTATATAGTGG GTCACCGAGGTCCTGTAGCAGAGTGGGCAA GCTCACTGCCTGCTACCAGCAGTTCATATG TTTTATGGTCTGCTGCCTGCTGGTGGTTATA GATGCTGTGTCGTAAGAGAAAAGTTCAGGGT AGCCTGGAGTGAATGGAGTTGGGGTATCAG GGAGGTCTTTGTACACTGGGGTGAGCTAGGC CTCTGGAAAGCTTCTGGGGGTTC	654	D	--
IM000321	CATGCTCCCAGGCACCAGGCTTGCTTTGCAT AGGTGGGACAGGGTCCCAATACTCAGCCTG GGGTGCCAATGAGGCTCAGGCCACACACCC TCTTGGTAGGAGTCACTGTAGTGGGGTCTGT GAGAGCCAGTAACTTGTGAGGGTGTGAACCT AGCTCAGGACAGAGGCCAGCAGGAAGCTTT CCCTACAGAGAGTGTTCCTGCTTTTCCTTTT TCTGGTTTGTTCCTGGGAAGGGAACAATTTT CGCTTTTAGTTGGCTGTATTATTCGCTACTG AAACCTTAAG	655	D	--

IM000322	CATGTATTAAGTCCCTCGTGAGGAA GGGT	656	D	--
IM000323	CATGAGTCAGAGGCTTCTACTCCAGTTAAAA CTGATCTGGGTATAGAATTGTGTTCTCAAGAA ATAGTAAGTTATAATCAACTAAGTCATCTCCT GTCTCATTTTTTTCTTCCAAATCGGGTCCTCG AATTGTTATAAGAAGATTCAATCAATCAACAG TATCCCTTTCCCAATTTGTGTGCTAAGTGGA ACAGGTCTTAGCACATCAATCACATAAAGTTC AATTAAGAAGGAATTTAAAGATCAG	657	D	--
IM000324	GCTATGAGTCTCCACTTGTAACAAT TATACTCAAACATATTCAGGACACAC TTGGGCTTCCTCCATCAAGCCAGGC AGGTTTGTTTTCTTGTTTGTTTGAGA TAGATGGATGGGCCAGCTTCATG	658	C	--
IM000325	CCCACCCCTAGCAACCAGTTCCTCCTCTGAA TGGAAGACATCTGATACCAACTTTGAGCTTTC ACATG	659	D	--
IM000326	ATCNCGAATCATTCTAGGCTTGTGG GACCATG	660	D	--
IM000327	ACTATTCTCAACAATAAATGAACCTTCTGGGGG AATCACCAATCCTGATTTCAAACGGTACTGTA GAGCAATCATG	661	R	--
IM000328	CCTAGGCACCCACCACAATAGTTAATCCATCT TTGAATTTTTGACCCAGTGTTGCCAAGTATTC ATTGCAACAGCTTTTCAAATGTTTTATTCTTTC CCAAATAAATTCCATG	662	D	--
IM000329	AGAGGCTACCCCTTCAAGTGGCTTGCCTAGT ATAGCTATTACAGACAGAGAACTTCCAGTAAT TTCCTCAAGCCACATG	663	D	--
IM000330	ACTCTGAACCTTGTCTTGCCTGGTATTTTTGC CTCTCTTATCCCATTTGACCCTGTACAGAAAAG CTGAGGAAGCAGGTGCAACCAGGCATCTCA GGCACCCAGTTAAGAAGTAGATGAAATACTG TAATGTACATG	664	D	--
IM000331	CATGATTTTCAGTTTTCTTGCCATATTCACG TCCTACAGTGGACATTTCTAAATTTTCCACCT TTTTAGTTTTCTCGCCATATTTACGTCCT AAAGTGTGT	665	R	--
IM000332	CATGAGACAGTCCCAGATCCCTCACCATAAA GAGCTACCATATAC	666	D	--
IM000333	CATGCGACCATCCATCAGGAGTTGGAGGTGC CATCGGCTCTGCCTTACAGAAAAGGAATCTG AGATTTAGAAACCCAGGTGACCCACTCAGG GCCACCGGGGCAGTAAAAAGAATCTAAGATC TAAAGTCAGTGAACTCCTCCCAACCAGCA	667	K	<i>Fgf3/Fg f4</i>

	GAGACTCCTCCCAGCCAGCTCTTGAT			
IM000334	GGGAAGCAAGAGGCAGTAAGAAAGGGGAAA CTGGGGAGGTAACCAAAGTCACATG	668	D	--
IM000335	CATGCTAACAAAGAATGGGGAAAGCTCTCTA GGCTTCCACCTTAAACAATGAGGAAGGGAAG AAGGAAAG	669	D	--
IM000336	CATGTTGGTGGGACTTTATGGGTATTGCTTCT GATATTACTAGGAGGCACAATCTCACAGAAA ACTCCCTGATCTTACAATCCTTCTGCCCCCTC TTTTGCAATGTTCCCTGAGCCTCAAGTATGGA GTTATTTTATAGCTGTATTCAATGAGACCAGA ATCCACAGGTATGC	670	R	--
IM000337	CTCACACAGATATGCATG	671	D	--
IM000338	AGAAGTGATCTTTCTTCTGTGTGCCCTGTCA CCCTGGGAGGCAATCAGACGGTCCCTCATG	672	D	--
IM000339	CTTTCCTTTTGTGTTTGGACGAATATTATTGAAA TATGTAGTGTGCATG	673	D	--
IM000340	CATGAGATATGATTTTAGATCTGAATCTTGCT TTTCAGGTGTCTTGGCATATTCAGAACTCGCT GTGGTGGGTGAACTGGGTTCTGATGATGCC ATTGGTGCTGGTTTC	674	B	AI5970 62
IM000341	CATGGAAAGGTATTTGGAAATAGGCTGTTTTG TGTGTAAGTC	675	D	--
IM000342	CCCTAGGACTCACCTGGTAGGAAAGAAGTAA TTCTTCCAAGTTGTCCCTGACATCCACAAGC ACATAGTGTGAGGCATG	676	D	--
IM000343	CATGCCATTCATACATACTGGCAATGGATATA TAGAAAATGAGACTCCTTCTAATATTGTGTGA TGACAGAT	677	D	--
IM000344	AGAAACCATTACACTGCCAGGTTTGGGGCC TGCTATGCATG	678	D	--
IM000345	GATCCCTTTAACTTCTTGGATAGTTTCTCTAG CTCCTCCATTGGGGGCCCTGTGATCCATCCA ATAGCTGACTGTGAGCATCCACTTATGTGTTT GCTAGGCCCTGGCATAGTCTCATAAGAGACA GCTATATCAGGGTCCTTTCAGCAAACCTTTGC TAGTGAATGCAATGGTGTGATCATTGGAGG CTGATTATGGGATGGATCCCTGGATATGGCA GTCTCTAGATGGTCCATCCTTTGTCTCAGCT CCAAACTTTGTCTCTGTAAGTCCCTCCATG	679	R	--
IM000346	AGGGTGGTCTCTGCAACCCAGGCTGGAACC CAGCACAAATAAATAGTTTTATTTACATAACCG AACGCGTGGCTCTGCGGCCACATTTGCGGTGC AAATTATTTACACAGTGATGAGGAGGCAGGA CAGGAAGGGGTGGGAGGAGGCTGAGGGAG	680	K	Wnt1



	GCATG			
IM000347	CATGTGTGTTCTTTTGTGATTGGGTACCTCA CTCAGGATGATATTTTCT	681	R	--
IM000348	CATGAGGCCAAGGGAGAGGCCAAATTCCTGTG TGAATCAATTATCATCTCACAGAGAACATACC	682	D	--
IM000349	AGTAGTATGCCACAGGGAGAAAAGGTATTTA TCAAAGGGACAGGAGCTAGTTGTGGTGACCT TACCTATCTGCTTGCCTCTGCCTCCACGGTG CTGGGATTGAAGGTGTGCACCACCACACCCA GCTTCAGATTTTTGTTTTATTATTGNGTATT CCTGTTTCACCTGCATG	683	R	--
IM000350	CATGCATATACAGGATATAACCTTTGTAAGTA AGAATAAAGCACATAAAAAATACTTTCAGTAA TATTGTCCAAACCACTT	684	D	--
IM000351	CATGTGTGTGTTTGTGTTTGC GGAGTGTGGG GGCGGCAGGGAAAGGTGGCCAGGCTGTCAC TCAGAGATCAGGATGACAGGCGCTCCCTCAT CTAGGCGCGGGAGCTCTGATTGCAGATTCTGA GAAACAAAATAGCAATTG	685	K	
IM000352	CATGAAGATGAACCGGGCTTGTCTCTGGC AACTAGGCTCAGAAAGGATAGGTCCACCAGC CGAGTAGCTGTCAGATGGAGCTGAAGACCTG AGGGAAAGAATGCTTGTGGGAAGA	686	K	<i>Wnt1</i>
IM000353	TCAGTTC AAGAGATGACACAGCCG CAGTCATG	687	R	--
IM000354	CAGAGACTGAAGGAAAGACCATCCAGTGACT GGCCCAACTTGGGATCCATCCCATTGAAAG CATCAAATCCAGACACTATTACTGATACCATG	688	R	--
IM000355	CCCTACAGTGACACTTACTCCAATAAGGCCA CACATCCTAGTAGTGCCAGTCCCCATG	689	R	--
IM000356	GGCCTCTATTCTCGGTT CAGATTAAGTACCTG GCTTCACTGAGAGCGGCTCTTTCATTCTAAA ATGGTTCTCATG	690	D	--
IM000357	AGTAGATGGCAGAGAATAATCAAACCTCAGGG CTGAAATTAACCATG	691	R	--
IM000358	CCAACCCAACAGCTGGGAAGGGTTGGAAGTA GCCCCGAGGCTGGTTAGTCCCCCTTCCAGATG GGGAGGTTAGACTGGGGCTAGCCAGGCTGC TCCACATAGACTTCCGATTGCGATTAGAAATG AAAAGAGGAGAGGAAAGGGAAAAGGAAGAA AGGCTACAAGCATG	692	C	--
IM000359	CATGGGGTCTGGAGCCAGCTATCAAACCCAG GATTGTCTTAAGTGTGGTGGCTTGGATGAGA ATGGCCGCCATAGGCGCATAGATTGAATTC TTGGTCCCTAGTT	693	R	--

IM000360	ACGGTGGGCTGATATTTTCTAGATCTCCTAGT GCCTATCCCCTATTATCATG	694	C	--
IM000361	CATGAATTTTGAGATATTCTCTGAAC CAAACAATATT	695	D	--
IM000362	GGAGAAATTATGCCTTAAATTAAAAAGCAAAT ATTGAAAAATTAAATATAATTTCCATTAAATCA TAATGGACCAACAACAGAACACATCTATCTAT GTATCTATCTATGTATCTATGATTTATCTACC TATCTATCTGAAAAGCAAAAACACTACATG	696	D	--
IM000363	GCAAGGACAACCTGACAGTTTGAAGCAACTAT TTTCATCTTGACTCTCACTCGGCTTTTAACGT CCATTGAGGAAACAGGCATG	697	D	--
IM000364	CATGAGAAGTCACAATTCCACCACTT AAAATCAGTGCTTGGAGGATACTGT AGGCCAAGAGGTAAGTAGAGGGGAC AGCAGTGCACGTTTTTCAAAGTGTG GGTGTGTGTTTGTGGGTGTGTGTCT GTCTGCCTGTGCGTGTATGTGGGTC AGTACAGGAAAAGC	698	D	--
IM000365	CAAGATAAACTCTTAATGGGATTCTAGGGAGT CATTCTGTAGAGAGCACTTGACTAGAAGGTT AAGTCTTAGATCCAGATCCCAGCACAAACATA ATACATCCTATACTCACACACACACACACA CACACACACGCAGTCCTCATG	699	D	--
IM000366	CATGTCTCAAAAAAAAAAAGAATCACTTGGA TTGTACATAGTAGTTAATAATATGTAATTAGTC TAACTGTGAAGGGGCACTTATTAGTTTCTACT ATGTAGTGTAATGAACTATGTTGCTATTAGA AATTC	700	D	--
IM000367	GAAGGTTGAAATCTGTAATCTATCTTCTATGG CATCATTACCTCTCTAATACAGCTGTAGAGA AAAATGTCTGAAGATTCGGTTCTACTCTCGTT CTTTGAGGTCTCCAACCCATG	701	D	--
IM000368	CATGGCTGGACTATAGAGCTCTAGCTTCAGT TGCTGGGATGTTCACTGCATCACCACAGAGA GGTTCTTAAGTGGTGATGGTGGTAGTGGAA AGGTGGACCCTCCAGACAAAGGAAGCACTCA CCACGACCCTGCTCACCTGTGAACCTTTCCT TTCAGACTGATTCCTGAGATCAGCCAGGCAG GGCTACCAACCAGGGACTCGTAATGAAAATT TAGGCATATGG	702	D	--
IM000369	CATGGTCTGGTGAGTATGGCACCAGATAGGA TGTTATGCCCGTTTCTTATCTCAAGAAACAAG GAATCTTGTTTCTTATCATTAAAGGAAGAAT AGAGCAGTCCTGGCTAAATGAAAGGTGGNAA AGTTGGTTTGAGTATCTCTTTCC	703	D	--
IM000370	AAAATCCAATACACATTCATG	704	D	--

IM000371	CCCTTTGTTGTGCATTTTCAGCTAATCTCATCC CTGTTTGGGTCTGGAACCTCTTGCTTCCC TGGCATCTAGGACTTGCTAGTGGCTACCCCC AGCTCCCCATTCCCCATTGCTACACACCTCT GTTCAAATTCCTGACCCTCTGTATATCATCCC AGTCTCTTCTAATACCTGACCTGAACCCCTT TTCCCTCCCTCTATTCTCTTCCCTGCAAGT CCCTCCACCTTCTACCTTCCATG	705	R	--
IM000372	CATGGGTCAATTTCTGATCTTTACCAAGCAACA GTGATGAATCTATAAATAGAACCATCAGTTCA AGAAACACAACCTTTAGATTCTTTCCATACCT TGCTTTTGTTCCTTACATCTTCCCCCTGCCCT GTGGTTTTCTTTAATCTTGTTTTTACAATCC AAATTGTATCCCCTTCTCTGTC	706	D	--
IM000373	TTGGGCCTTTGCATACCCTGTTCTGGCTAAG ACAATTGTCACCTGACTGGGCATG	707	D	--
IM000374	AAGTGGATGTTTCTCATTTTCCATG	708	R	--
IM000375	TATAAGCAATCCCAAAAATTCTACCTGGGAAC TCCTAGAGCTGATAACACCTTCAGTGAGCCA AGTATCTGGGTATAGGATTAATTTAAAAAAA TAGAAAATCAGTATCTCTTACATACAAATA ACAAAAGGGCTGAAAAAGAAATTAAGGAAAT AAAACCCCTTCACAATAGCCATAAATAATATA ACTATCTTGGGATAACTCTAACCAGGCAAGC AAAAGACCTGTATGATCAAATCTTTGAAGAAG AAAATTGAAAAAGGTATCAGAGGAGGTAAAG ATCTCCCATG	709	R	--
IM000376	CATGGGCTCTGCTTAAGAAACCCCGGAG	710	C	--
IM000377	CATGCTTTTAGGCCTTTTCACGATCTTANNGG GGACCGNGAGAGNTNGCTGCTGGATGATCT CTGAGAGAGCTTATCGTCCTCAAACCTGCTGA TATTCAAGCTGTTTCGCAGCTGCAGCAGCAA AGTCCCGGTCTTTGTACCGATCTGTGAACA GCAACAATGAGCACCTTTCATAACAGACAGG AAATGGATGCT	711	A	<i>mDal1</i>
IM000378	GGCGTACCTGTGTATATGCATGCAT G	712	D	--
IM000379	GTGCTAGGCTCACTCAAGATAAAATT TGCTATTTTCAGCTCCCTGGATAATAA AATCTATCCTCTCACAGCTGTGACTC TCACAGGGGTGCAGGCAGGACGAC ATCAAGAGAGTGATGGCCTCTAACA AGTGTCTGCCCCACTTCCTCTTCCGG GTCAAAGACTAGATCTAGACTGGTG GGGCTGTTGATTCACTATGAATGTGC CTGACACCATCCCACACTTAGCATCA TAGACACTTGGGGGACTGGTGATAC ACTATGATGCCTGACACCATCCCACA	713	D	--

	CTTAACATCATG			
IM000380	CTATCCCGAGGGTGAGGGCAGTTCT ATGCCAAGGTTCTCATCACAGAGATA CAGAGGAAGCTGGGCCTGTCTTAGG GTTGGCTGTCTGGAGATCCTGGAGC CCTGGAGGTGGGTAGCAAGAACAAA GGAAGTACTTCACCTGATAAAAAACAG TTCCCAGAGAAACACATATACGCTTC ATATACAGGAGTGCGAGTGTGTGTG TGCGCGCAGAGAGGCAGAGGCCTG GAAGTCAAAAGTTCAGGGCCAGTTT GTGTGCATG	714	K	<i>Fgf3/Fg f4</i>
IM000381	GGGGTTGACTAGAAGAAGGAGGCGATTAGG GTGTATCATATGAGAGAAGAATAAAAGGA AAAAATAAATTTACAAGGATTA AAAAGTAATTA CATACATACATACATACATACATCCATACATA CATACATACAAGTTAAACTGTTATGGTAGCAT G	715	D	--
IM000382	AGGATGATATTTTCTAGTTCATCCATTTGCC TAAGAATTTCTTGAATTCATTGCTTTTAATAGC TGAGTAGTACTCCATTTTGTAAAGTATACCATA TTGTCTGTATCCATTCTCTGTTGAAGGACAT CTGGGTTCTTTCCAGCTTCTGGCTATTATAAA TGAAGTTGCTATGAACATAGTGAAGCATG	716	R	--
IM000383	CATGCCTGCAGGTCACAGCCTTGCGCGCCTC CAGTGCCCAGCGTTCAAAGTGACACAGACTC TGTCAGGATGGTTCAAATGCAAATCTCTGCAA CTGCGTTAGCCGCTTCTAACCAAGACAGAAA GCTGCCGTCTCTGTCTTCGTGTCTGTCCCCA TACCCCATATCGGGTAGCTTTTCTTTCAGCAT TGTCCAGACACCATCATATGCCTACATCGCA CAAGTTCTCTGAGGCCAGATAATTGGCAGCA CTCCTGTTGTGTGCCGAGAGTGCAGAAAAGG GCTATCCCAGAAAAGGTGTGATCTGGAAAGAA GGAAAAAAC	717	D	--
IM000384	ATCTTTTGGCCAGAGCAAGCAGGGACTGAGT GAGCAGAGGTGACAGGAGCGAGCAAGGCTG ACAAAGTCTTCCATATTCCTACTAGGATGACC CATTAAGCCCCATTAAAGCATTCCATTGCTT TCCAAATACAAAGTCCCAAAATCCACATTCTT TCAAATAAAAGCATG	718	C	--
IM000385	TTAACATATGGTTTTTAAAAATCCATAATGAG CATATGATAGAGAAGTCATCAGAGCTCTTCA GCTCCACATCATCTGTCCCCAGAAGTATTACT ACTCCTAACTTGCTGAGCCAAGGCACAGATA TTCTTTGTGTAAGCATCTCTTCTTATCCTGT GTTGCCACGCAGGAGCACGCACACTGCTTCC TGTCTGAGGTTGTTCCATATCAGCATG	719	D	--
IM000386	CATGCCAGGGCTTGAATTAACACAAGTGCCC	720	D	--

	CAGAT			
IM000387	CCTGTCTGTATATGCACATG	721	D	--
IM000388	CATGGAAATGAGAAACATCCACTTGACGAC TTGAAGAATGACGAAATCACTGGAAATCGTG AAAAATGAGAAATGCACACTGTAGGACCTGG AATATGGCGAGAAAAGTAAAATCACGGAAA ATGAGAAATACACACTTTAGTACGTGAAATAT GGCGAGGAAAAGTAAAAAGGTGG	722	R	--
IM000389	CATGAAGGTAAATTATGACCATCAGGGTTCA GACCTCAGCTCGACCGGAGACCAGCCTGCA ANTCCCCACAGCCCTCCCTAAAGTGGGTAA AAGACAGAAAAGAATTAATATCTGA	723	R	--
IM000390	CATGCACTAGCAAGATTTTGCTGAAAGGACC CAGAT	724	R	--
IM000391	GACACATACACACACATG	725	D	--
IM000392	GTAATGTATTAGGTTGAGAACTGGCACTGCT CACTTATGTTACAGTTGTTTGGGTAAAAGT GAACCAAAACAAAAAGCAAAAGAGCCAAGCA GCAGAGCAGGGAGCAAGGGGCTTGGGAAA ACACTCACCTCTGTTGTGTCTTCTTAGCTG TCAGGGCATTGAGTGGCAAGGAGTGGAAAG GAACTTTGGGCATTCCGAGTCAGGAAAAGT TACCAAAATAACACTATGGAGGTTAGCAAGT GTTCTAGAGGGCAGAATAAATACATG	726	D	--
IM000393	GTTTAGGTCATTGGTGGTACACTCTCCAAGG ACAGTATAAATTGATTTTTTCTGTATCCTTCT TTGTTCTTGGCCATAAGGCACTTGGAGTGCA TTAATATGTACTTATTACTATGTCTTTTCT TGTCTTTGGCTTAAAAGAAACAGGGTCAAGT GACCATG	727	C	--
IM000394	AGTTTTCTTTAAAAAATAAAGTAGGAATGAA ACTGGAACAAAAATGCAATAAATTTTAAACCA TCACCGCTAAAACATG	728	D	--
IM000395	CATGATTTTCAGTTTTCTTGCCATATTCCAC	729	R	--
IM000396	GAGAGGAGCCTGGGGAAATGAAGGT CCAGCAACAGGCCCAAAGTGGGATC CAGCTTAAGGGGAGGCCCAAGGC CTGACACTATTACTGAGGCTATGGA GCACTCATAAAAATGGACCCAGCAT G	730	R	--
IM000397	CATGGCAGCCTTGGAGTATCAGGCT GCTGTTCCCAATGTGGGATGCAGAG GGCACTGCCAGCCTGGTTATCACGC ACCACTGTCACACAGGGAAGCGCCC CCTTCCC	731	D	--
IM000398	GGAGTTCTTCTCTTCAATAACAGAGTAAATTC	732	D	--

	TCCCTCAGCAGTTCTCCCAGGAAACCCATAA CCTAGCCATG			
IM000399	CCTTAGATGTTTGTCTAATCGACAAAATACTT TATATGTGAAAAGGAAAAGCATG	733	D	--
IM000400	AATAATCAGATTTCCAGAGCTCCCAG GAACTAAACCAACAACCAACGAATAC ACATG	734	R	--
IM000401	ATCCAGTAATCATTTCATCTTATTGTTTCCACA CAGGAAAACCTGTAATAGATGGTTCATCAGC TTTATTTATAACTTTCTATCTTGAAAGCAACTG GAATGCCCTTCAGTAGGTAAGCAGATACT AGGCTCACCTCACTATAGGCACAATGAAAG GAATGAAATGTCAACTCACGAAAGGTAAGTA CACATG	735	D	--
IM000402	CCTCGCCATATTTACGTCCTAAAGTGTGTAT TACTCATTTTCCGTGATTTTCAGTTTTCTCGC CATATTCCAGGTCCTTCAGTGTTTCATTTCTCA TTTTTCAAGTTTTTAGTGATTCGTCGTTTTT CAAGTCGTCAAGTGGATGTTTCTCATTTTCCA TG	736	R	--
IM000403	CATGCAAGAACAGGACAAATGTCTGTGAAGA AAATGAGTGAGCGTGAACAGGAGGTCAAGGA TCCGGTCCCAGGCAGCTCTCAGTCTGGGCAA GCATTTCTAACTTTGCCTTCCTCCTGTTGG GGGTGAAGGTCTG	737	K	<i>Fgf3/Fg f4</i>
IM000404	AATAGGAGTAGATGAGAATGAAGATTTTTCAA TTTAAAGGACCAGCAAATAGCTTCAGCAAAT TATAGAAGAAAACCTCCCATACCTAAAGAAAG ATGCCCATG	738	R	--
IM000405	CATGCAGCCCCATTAGTGATTGATCCTGTTC CATATAA	739	D	--
IM000406	CATGGGCTCTCTGCTGATAATGCTG AGGCTGTTTGTGCTGTAGTCTGCGC TTTTTGCCCCCTCTCAGAAAACTGT ATGTCATAGGAGTTGCTGGCTATTG GGTACATAAGCAAAGCCACCCTATT GTGCCAGTGCCTTAGACAGTGAGAC AAGAAAGGCCCTGGTTAGAAATCTT ATCAGGACTGGGAATGTAAGTCAAGT GATAAGAGTGCTTGCTTAGCGTGCA CACAGCCCTGGGTTCAACCGCCTAG TACTACAGAACTGAGTGTGGCTTCA CACACCTGTAATCCCAGCACTTGGA GAGATAGATGCAGGAGGATTAGAAG TTCAAGGTTATCTTTAGTCACATAGT ATTGGTAGCCAGCCAGCCTGGAATA CTTGAGATACTTACAGGAAGGAAGG AAGGAAGGAAAGAAGGAGGGAGAG	740	R	--

	AGGACAGGAGGAAGGAGATAGATAT ACACAGAAAGAGACAGAGAAACAGA GATTCAGGAGACACAAAGACATACG GAGACACAGTGAGA			
IM000407	CATGTGGTTGCTGGGGATTGAACTCAGGACC TCTGGAAGAGCAGTCAATGCTCTTAACCGCT GAGCCATCTCTCCAGCTCCCTTTTAGACTTCT TAGTAGCAGCATTAAATTCTTGCTTGGTTTCAG TTCTGACAACCACAGCAGTCAGGAGTTTGAG TAAGAGG	741	R	--
IM000408	CCTCATAATGTTTGTTTGAGCATTTTT TTAAACCTAACTTGTCTTTTGCTTAT CTATTGTGGTTTCTTAGTGTGTGTGT GTGTGTGTGTGTATGCGCGCGTGTG CTCTGGTCTTCGTGCACATG	742	D	--
IM000409	ATTTGTGACATCTTAGGAGCTTAGGTTGGTCT TCGAGACACAGGGCTGTCCCTGTAAAGCAGG TTCCATCAGTGACTCCAGGGTTTAGCAGTTC AGTGGCGTAGTTTTCAGACTGCTTAAGATTTT TCAAGGGCTAGGCGTGGGGCAGAGACCCTG CAGACCCTGGCTAGAACAGANGCCCTGGGA GACAGTTGAGGGTGCTCAACTGTGGAGGACA TG	743	K	<i>Fgf3/Fg f4</i>
IM000410	CATGTATGCACAACCAAACTTATAAATATGA GAATTCACCTATAGTCCTAGTCCTTTAATACA GAATTTAGCATTCCGATATAAAACAACAGATT AAACCCCAACAGTTAGAATAGAGCAG	744	D	--
IM000411	AATAGGAGTAGATGAGAATGAAGATTTTCAAC TTAAAGGGCCAGCAAATATCTTCAACAAAATA ATAGAAGAAAACTTCCCAACCTAAAGAAAGA GATGCCCATG	745	R	--
IM000412	CATGCACACCCTACTCCTGGGTGATCGTACC AGCTCCAGCCTCTGTTCTGCACGCTGTGCCT TCAACCTGGCAACCTCC	746	K	<i>Wnt1</i>
IM000413	CATGAAAACCTGTCTCAGAAAACAAAACAC GTTGAGAGCCAGCATAGAAGCCATAGGAGGT AATGTGTGTGTGTCTGTATATATGACAAGAGC AGACCTGTGCTGAACCAGTTAACTACTTTTG	747	D	--
IM000414	CATGCTACTAACCAGTTGAGGCAGTACCAGT TGTTGAAGATGCTGTCTTTTATCCAATGGATG GTTTGTAGCTCCTTTGTCAAAGATCAGGTGATC ATAGGGTGTGAGTTTATTTCTGGGTCTTCAGT TATATTCCATTGATCTACTGGCCTGTAATTGT ACCAATAC	748	R	--
IM000415	GGTTAGGAATTCTGGACAGTTGGTACTTGGT TTGAATATAGTAGGTGACAAGCTGTGCCTTG AGTGGGGTGGCAAGCAGGGTCTCTGCAGC	749	C	--

	AGGATGCAGTGTACATG			
IM000416	CATGAAAATGTTAAGTCCTGACAGACAGGGT GCCATCTGCCAAGAATTTGAGTAATCTAGAAA CAGAAAT	750	D	--
IM000417	CATGGGGTTTTGTGGATCTG	751	D	--
IM000418	CAGAACAAATAAGCTGGAAAGGATGAAGCAG CCACAACATAACTGCTGTTGGCTTCTTTGTGT ACATTTTAAACCTTCTCTGAAAGAGTGACCA ATGCTTTTAACTGCTGAGTTATCTCACCCGAC TTACTTTCTCTCTCTCTCTCTTTTCTTCTT CCTAAAATTAATTGTGTGTGTATGTGTGTGTG TGTGTATGATTAGAAACCTTTTATGTGGTGG TAGAAGACCATCTGCAGGATTCTG	752	D	--
IM000419	CATGGTCCCACAAGCCTAGAATGATT CGTGGAT	753	D	--
IM000420	GGGGTCCAGGAGAGAACTTGAGTC ATG	754	D	--
IM000421	GGAAAGAGATACTCAAGACCAACTTTACCAC CTTTCATTTAGCCAGGACTGCTCTATTCTTCC TATTACTGCTAAGAAACAAGATTCCTTGTTTC TTGAGATAAGAAACGGGCATAACATCCTATCT GGTGCCATACTCACCAGACCATG	755	D	--
IM000422	GTCCTTCCCAAAGAATAGTGTTAACTGAGCTC TTTGGGTGGCAATAAATGAATTGCTCTGGTG GGACAGGCAGTGACATATGGGGAGGGGGA GACACATG	756	D	--
IM000423	CATGTTCTTACTTCTTGTTG	757	D	--
IM000424	GGGTATATGAATTATATATATGTGTGTATAT ATGTATACAGGCATG	758	D	--
IM000425	CATGCGCCCTAAGACTCATCTCCACGAATGA CGTGACGACCTAATTGCATTCTTCTAACCCA CTGATTAGGCAAACCACCCTCAAAGGGCTC GCTGAGTTCCTCTTCGGGAAGAGGTGTGTTG AGTACGCTGGAATGGATATTCGAGGGCTGAG G	759	R	--
IM000426	CATCTCTCGAGCCCTTGCCCAGCCTTTTTCT TAAAATTGTATTTTTAAATTTATTTTCTGTAC ACAGGTGTGTGAGTGTGAACATG	760	D	--
IM000427	CATGTGGACCTGGGGGCTAAGTCAGGGTGA AGCTTCCACAGCTAAGTGGCTGGAGGCTGCC CTAAAAGCTCAGGAGGCACCGCAAGCAAGC CTTGAAAAACCTTACCCACCAGCTTGACCTTA GACTTCTGGCCTTCAGGCTGTGACAATACAT TCCTGCTGTTTAAAGAACCATATGGTTGGTGA TGTTTTGTTTGTCTGTTCTTTTGTGTTGGT GTTTTTGTTCGCGGGTGTGTGTGTGTGTG	761	K	<i>Fgf3/Fg f4</i>



	TGTGTGTGTGTGTGTGTGTGTGTGTTGCAGT GCTAGAGATAAGATCTGA			
IM000428	GTCTAAAGTTTTCAAATGATGGATAAGTTGTT AAACCTCCTTTAAGATCTCAAGCACAAAAAGA AAGACATCAAATACGAATAGTAGAAAGGAAA GGAGATTTGGAAGTGTAGAGGCCCAAGAGTCA TAAAGAGAAGAATTTAAACAAGTGTACCCACA AATTCATTAGCATAGATCAAGTAGTCCATTTT TTCATG	762	C	--
IM000429	CATGTATGTTCTCGATGCCTTGGCCT G	763	D	--
IM000430	AAAGACATTAAGTCTTGAGAACCAAGGGGTA GGACAGTATAGACTGAATTTTGCCTCCCCTCT TCATAAGTTGTCACTGCTAACCTCATTTCAGA ACTTAAGCATATAACCTTCATG	764	D	--
IM000431	CATGGAGAACTAGCAAGAGCAGGATGGCGTT TCTCTAGAATGCCGTATAG	765	D	--
IM000432	CATGGTGACTTTCCATCTTTAGAACCATAATC ANGTTTAAT	766	D	--
IM000433	CATGCTTATATCCCTCAAAAATTTTACAGTTAA ACTGAAAATGCTTACTTACTTTTTTTTCTTACT TATATCTAGTATCGATAAGAACTGTCCCAAAG GACAC	767	D	--
IM000434	CTGGGTCTTAGTCCTCTGAGGTCCCTAGCAC ATCAGAGGTTTCATCAGTTCCAAGAGATGACA CAGCCGCAGTCATG	768	K	<i>Fgf3/Fgf4</i>
IM000435	CATGGAGAATGCACAGTCAAAACGCTTGCAT CCT	769	D	--
IM000436	CACCCCTCCCGCCTTACATCAATC CTGGGTGCACAATGGGACTGTGGAT GACTGATGTCTGCGCAAACAACCTTG CGGGGAAGTCTAGCTGACAAACGCT CATG	770	K	<i>Fgf3/Fgf4</i>
IM000437	ATGTATCCAATGGCAAAGCACGGGGGAGGCT TCATCTTGAAGAGAAGAGTGCTCTTGGTAGG CTATCCTTTTTTTGAGACAACTAGAAATAGGA GCATTTCAACAATCTGGACATATGTCCTCCCA CAAGAACTTGTTGAGAATGGGTCTGAATTAAC TGGAATAAAAGTGAACACATTCTCCTATACA CATG	771	D	--
IM000438	TCACTCCATTTTAGTTCAAATGCTAC AACTCCTTTGAGCACCCTGTCAATTT CAAGACCTTATTCTGTGAATACCATG	772	C	--
IM000439	CATGCTTAGCCCAGGGAATGACACTATTCGA GGTGTGGCCTTATTGGAGCAGGTGTGGCCTT GTTGGAAGAAGTGTGTCACTCACTGTTGGGG	773	R	--

	TGGGATTTGAGAGCTTCCTCCTAGCTGCTTG AGGATGCCGGTCTT			
IM000440	CATGAGCTGGGTGAACGACAGCAAAGGTTTG TTTCTCTTTTAAGGAAGACAATGGTGTGAAAT TGGTTGATCCTTTGGGGGAAATGTTGGCCCC TT	774	B	Mm.202 45
IM000441	CATGATCTCACTGTGAGGGCTGGCTACCTTG GAGCTCACTGTACTGAAATATTCTGGCCGATT GCCTCTTCGCTGGGTTTATGGGCACACACAG TACTTGTCTATGAGTCTTTGTTAGGCTGAGCC TAGTGGTGCAGGCCTGTCATCTCCCCTACTT TACTTTAGGCTCTGAGGCAGGAGGAT	775	D	--
IM000442	TCTGGTAACTTGGGGGTCTGATAAAA CAGTTGGGGGATTTCTTTTCTTTTCG CGTCTGAAGCCAATGTTATTACAGGT GTGTGCTTGTCTCTCCACACCCTG CCCCTGTTGCCTAACACACGCGGCA CACACATG	776	D	--
IM000443	CATGACTCTTCCTCCAGAGTTAGAGGTGGAG CCAGGACAACTCTAAAGAAAAGAAACCCCA ATCAAAAAGGGAAGCTGGTATCATCCAACCT TTAAATTACTCCACATCCCTCCAGAG	777	D	--
IM000444	CATGTCTGTCCCAAAAGGAAGTTCCTTCCTCT GTCCTCCACATCTGACCAGCACCATCATTCA ATCTGCAACCCAAACCAGACATTTACATCATC TATGCCTCCTTTCCTGCTTGTCTCCCCTCAAC CAGCACCCAGCAAGCTTTCAGGTATCCCCTT AGTGTGTGTCAGGATCTCTCCAGTCTCCAGA CCCCAATTCTGTTCTCACTCTACACTGCTAGC	778	D	--
IM000445	AAAGCTAACTTCTCATCACCTACCTAATAGCC TGAGAGCCCTGTGTAGAAAAATTAAGGAGTT TAGTTCCTTCATG	779	C	--
IM000446	CATGCAGACAAAGTAAATAAGAAAACAAATTA AATGTAGGCTGGACGGATAGATGGT	780	D	--
IM000447	CTCAGCTCCTAGGCAACACTTGTAGACCCAC AGCCCCCTTCACACACACACACACACACAC ACACACACACACACACGCGCTGGGGATCCAAC CCATCTCGTCCTTACACGTGCTCTACCATCAC ACCACACATTTCCAGCACTTTTATCTGAAGTG TTTCCTTTTATTTGTGCATG	781	K	Wnt1
IM000448	CATAACCACTATAACCAGCCTGCTTACTTGGC TTTGTTCGAGGGCTTTTGTTTTAGAGCTCTT TCTTTTACCCTTCTCCGTGTGTGTGTGTGTG TGTGTGTGTGTGTGTGTGTGTGTGTGTGTCT GTCTGTCTGTCTGTCTGTCTTAGTGTGTGTAC ATG	782	C	--
IM000449	CATGTGGTCCACGGTTTTACTTTACTAGGGA	783	C	--

	GCAACCTGTACCACAGGGAGAGAGGCCTAA GGACAGGAAAGGAGCTGACCCAGAAGTAA AAGGCACACACCATTCTGCCAGCACTTCCC			
IM000450	CATGTCCTACAGTGGACATTTCTAAATTTCCC TTCTTTTTCAGTTTTCTCGCCATATTTACGT CCTAAAGTGTGTATCTCTCATTTTCCGTTATTT TCAGGTATCTCGCCATATTCAGTTCCTACAG TGTGCATTTCTCATTCTTACGTTTTTCAGTG ATTTGTCATTTATCAAGTCGTCAAGTGAATT TTTTTCATTTTCTCTGATTTTCAGTTTTCTCGC C	784	R	--
IM000451	CATGTTGCCTCAAGACAGATCTCCACTTTAAA GACATACCTAAAGGCCTGGAAGCTTAGTCAA TTAAGCTTTCCTGCCAGACACTCCTCCCTG AAAAAGGTATTTAACCTCAGGCCACCCCTGA GAAGTGGGGTATGATTTTACTCATCCACTTTC	785	R	--
IM000452	CATGGTTTCTATTACTGTGTTGAAGCACCCCTG ACCAAAGCCAATTGGGGGACGAAAGGGTTTA TTTGGCTTAACTTCAAATCAGTGTTTATCA TTAAAGGAAGTCAGGGTAG	786	R	--
IM000453	GCAAGTGTGAGACGGCTCTCAGGGAGATACA CATAGCTTTATTGGATAACTGCAGCTTGAAGA CATG	787	D	--
IM000454	CATGTACCTATGTGTGTGTAACATTTGCCTAT TTTCACACAGTTAAGAAAGCATCGTTATGAAA ATCATTACAACCTTTCAGATAAACAGATCCAC TCAGCCACAGAT	788	D	--
IM000455	GCCCTTCTCTCTGAACTTTTCAGTTCCTGGAT AAAGTCAGTGTTCCACCTCTATACCTGACTAG TTTTCTAAATTCTGAGTCAAGCATATTTCAT G	789	D	--
IM000456	GACCTCGTGGGCGGGCCTGAGGAGACAGTG CAGATGAGGTGTCAGTAAGGAGGATGCAAGC AAGAAAGATGCAGGAGATGATGGAGAAGCTG AAGAAGGCACTGAAGAAGGCACAGGGAAGA AGAGTGCATG	790	D	--
IM000457	CTTGCCGTTGAGAGCGTCCAGATCCCCTGAC TTGAGTGGGTCCACCTTGTGTTGGTTGGTTC GCAGTGTGCGGCTGTGGAGCCCCAGGCCTTG CATG	791	C	--
IM000458	TTCTTATCCACTGAGCCACACTGCTAATACTG TGATGTCTTTTTTAAGACTCACCATG	792	D	--
IM000459	GGGTTCAACACATTTTTGGAGATTGATCAAAA TTAAAACATG	793	D	--
IM000460	CATGAAGGAGAGTCTGAGGCTACATCCACCA GGCTCTATGATCTCCCTCTGCTGCATCCAGG	794	C	--

	ACATTCTCCTTCTGGATGAAGATGATGCTGG CGCTGGCGCTGGCGCTGACGCTGATGCTGC TCGCTTCTGCGTCCT			
IM000461	CCTTGTCTCCTCAAATTACAAAACCTCCC TAGGGTCTTTTCTCTGGGCTACAAAA TTCTGCAAATGGACTCAGGAGGAAT CAATGTGGAAATTTCACTTTGCCTTC CCAATCAGCAAAATAATGTTTGCCAA AATCGTTAGATTTCTTTCCCCTAAGT AGGCTACTGCCGACTTGAAAGCAGT GGTTCCAGAACCCGAGCCCAGGGG CTGCCACTTCCTATGCATG	795	B	AI4269 08
IM000462	CCCTTGTCTCCTCAAATTACAAAACCTCC TTAGGGTTTTTTTTTTGGCTNCAAAAT TTTNCAAAGGGCTTCAGGAGGAATA ATGGTGGGAAATTTACTTTTGCTTTC CAATCAACAAAAAATGGTTGGCCAA ATCGGTAGAATTCTTTCCCTAAATAA GCTACTGCCGACTTGAAAGCAGTGG GTTCCAGAACCCGACCCAAGGGCTGC CCTTTCTATGCATG	796	D	--
IM000463	CATGTATCTTAAGAACAGAGCCAGTGCTCTC CCTCTCCCACTTGAT	797	D	--
IM000464	CATGCAGANTAAAGTACATATATGTAAAAAT AAAAATAAATCTTT	798	D	--
IM000465	GTGCTCTCCCTTGCCTCTCCTCTCCT GAGTTTCTCTGTAGGTGTAAGGGCT GGAGGTGGGCCCAAGAACCAGAGAT CAGAGGAGGGAACTTCCGGAGCAGA GGCCCTGGGAGCAGTGTTAAGCAGG CTTTGGCCAGGTCTGGAGGTGTCCA GGCAGGGAGGTGGAGCTGGAAGAG ACCAATTAGTCAAACGGCTGCAATTG GCCATTTGGAAGCAATTAACAGGGT CTCCATTACCATATTATGCCCCTCCA CCCCCTCCACACTCTACTAGGCTCT GCTCTGTATGGAAGGGGGAAGGTGG AGGCTCANCTCAAGCCAGGGAGACT ACAATGGAGGCCCAAGTGTCTCGCCAG GATGCACACACTCAGGCACCCTCCG TGTGAGGAGGGGAGGGCAGGGCAG CATCTGAAGCAACCTGTCATTACAG CCTGANAGANGGTGGGAACAANGGC TTNCAAAGCCAAGAANGCANGTGGN TAGAAATGCANGAAAACCTCTCTGGT AAGAAAGGCTGAANGAAGCAGCTAG GGTTGTAAAACAAGANCAT	799	K	<i>Fgf3/Fg f4</i>
IM000466	CTCCCTCTCCCTCTAGCTGGCCTAGCAGGGG CCAATACAACCTGCAGGGAATCAAGGAAGAGC CTTTCTCTGAACCTGCTGGATGCCCCAGTC	800	B	AI5500 57

	CAACAGCAACTCCCACCTTGCCCTGGCTTGGT TTGCTCCACTGTCCTGAAGGCACAGTGTGAT ATCCCAGACCTCCAGCGAGACAGCCCAACCT GCAAGCCCTGATGGGAGGGGTGGCCTGAGA CAACAGTACCTACATG			
IM000467	CATGGACTCCAGGGTCAGGGTGTAAAGAAAA GGTGGAGCCTGCTAGGTGTGGTGACACACA CCTTTAACCCCAAGACTCAGAAAGCTGAGGC AGGTGACTAGCCAGGAGTTCAAGGTCATCTA GTTTCATCAGATCTATAGAGTGAAACAGCCAG GCTACATTTGAGATC	801	K	<i>Fgf3/Fg f4</i>
IM000468	GCTCAACACTTAAAAGCGCCTGCAGAGGGGT GGGGGTTTAAATCCCAGCACACACATAGTGG CTCAGGGAATCTGAAGCCCTCTTCTGGCCAC TGCCTGAACTGCATG	802	D	--
IM000469	GTGGGAAGCTATACGAAAGTAAACACACTC TAAGAAAGAGAACAGGCTGCCTGGGAGAGG GAGGTGCCAGGGGCTTAGACAGGAAGGTAG TTTTCAAAAAGTGAAGCTTAAAGCTATCTGAA TGAATGATACAAAATAAAGAAAGACACAAGAA TTTCCAGTCACCTGAGATATCTCACACTCCTG TTCTTTCAACCTTCTAGCTGAAAGGAGAAAGA GCCATG	803	D	--
IM000470	CATGGAAGGAGTTACAGAGACAATGTTTGGG GCTGAGACGAAAGGATGGACCATCTAGAGAC TGCCATATCCAGGGATCCATCTTATAATCAGC CTCCAAACCCTGACACCATTGCATACACCAG CAAGATTTTGTGAAAGGACCCTGATATAGCT GTCTCTGTGAGGCTATGCTGGGGCCTAGCA AACACAGT	804	R	--
IM000471	CATGCTTAGATTGACCGCAATATGTGTGGTA CTCTTCAGACTTTTAAAGATTTGCTGAATATC CTATCCCCTTAAATTGTGATCACCCCTAGCTA GATCTAATCTTAGATCTCGAAAGTTCTACAAT TTGCCTCAATTTGATTACTGTTTTCTCCTTG AAGAC	805	D	--
IM000472	CTTGCCTTGGGAAGTGAGGGTTCTAATGAA GGTTGCAAGCCTGTCCACCCAGGGCCCTGC TAAAGAAGGAATGGTCCCAGCCTGTTTTGT CCCCTCTGTGGCTTCTTAGTTCTGGACACTG AGCCAGTCTGGGCAGCAGGCAATTCACACTG TGAATTTCTGTGGAAAGCATTTTGGGGTTCT GAAAGCCCTGTACATTCTGTGTTAAGGACAG AGGGCCTCCTGCATG	806	K	<i>Fgf3/Fg f4</i>
IM000473	CATGGGGGCTATGTCCTAGGGTAGACACCCC CTTTATCCCTCACCTCCTTCCCTGTCTTAGCA GTGGTGTCCCCCACTGTGACTCTACTGCATC TGGGAGCTGTCTCCCGGGGGACTTCCTCCT GCTGGAGTGAGTAGGTGGCTAGGGCGAAGC	807	K	<i>Fgf3/Fg f4</i>

	CTGTGTAAGAGGCAGGAGGTGTTTTGCACAA CTCCAAAGGGTGCAGATCCTGCTGGCTCCAG CTTCCCAGGGCCAGACCCCCAAATACCCCTC ACCCAGC			
IM000474	GTGTATGTTCTCTGGTGAAAGTGTTAACCAG CTCACTCCGTGAAGAGCACGCTGCTTTCAGA TCAGTGTTTCAGAGTCTTGAATAATTGGTTTT AGAATCATAAAATTGCAGTCTTTACAAAGGA CTGGAAGTGACTCATG	808	D	--
IM000475	CATGTGAATTCTCTATTTGCAATGTGCTTGGT TCATACTTCCATACTCTACCCAGAGCCTGTTA GAAAAATCACTCTTCCCCACCCTATTCTTCAC CAGTCAATATGTATCTAGTATTCTAAACTTCC TCCCTCCTAAGGCAGTGGGGAAG	809	D	--
IM000476	CATGTGTAATCTCACCATCAGAATTATGAGCA ACCCACAATTTCTTCACATTTATAACTGACCC AGTCTGAGGTATTGTGCCTTTAGCAACAGAA ACTGAACCTCAAAACAATCGGCACAC	810	C	--
IM000477	CCATATCAGACCAACCTTCCACACAACAGT AGGCCACCAGGTGGGGGCAAAGTCCTGGGT AAGGTTCTTGGAAGTGAATTTGAATCCCAA TAATAATGACTGTGTTATTTGCTCATG	811	D	--
IM000478	TAAACCTTTAGGGAGCTGATAAAATCTATC AAAACAACACTCTGTCTCTCGTATCCAGCCAT CCATG	812	C	--
IM000479	TCTGCCAGCCTTTGCTTCCCTGGTAAC AGGATGCTAATTAGAATTCATG	813	B	AA1177 84
IM000480	CATGTAAAAAAAACCTTCATTAACAA CTACAACAAAGCAGAGACCTTGGCC CTTGATTGGGGCCCCTCTGAGAGC TATAGGCTGGGATACTGG	814	D	--
IM000481	GTGCGTGATAACCAGGCTGGCAGTGCCCTCT GCATCCACATTGGGAACAGCAGCCTGATAC TCCAAGGCTGCCATG	815	D	--
IM000482	ATGTCAACATTGAGTCCAGTAAGGACATCGT ATATGCTGGTCATTATTATAGCTCTAAGGGT CATACATGAGACAGACCACCCCTTACCCCC TCCCCCGTCTGGGCTAAAAGCAGACACACTG GGTTGGTGAGAGAGCAGCAG	816	K	Wnt1
IM000483	CATGAGACAGACCACCCCTTACCCCTCCC CCGTCTGGGCTAAAAGCAGACACACTGGGT GGTGAGAGAGCAGCAG	817	K	Wnt1
IM000484	CATGAGAAAAATTTGTCTCTAATTCTCTTTGT GAATTTTGTGTGGTTTTGATATCAGGTGATT GTGGCCTCATACAATGAATGTGG	818	R	--
IM000485	CCAGTGAAGTAAACCCAGCAGGACCCTTTAC	819	D	--

	AAAGCCAGGACATG			
IM000486	TCGGGGGAAAGTTATTTTATACCTTCCCGCT CTGGATTAAGGGAGGGTAGGAAAGGATTGGA TGAAGCTAGAGACAGAGTGGCAGGAAGGTG GTAGACCTGAAATTGTCAGACAACCACTTATC GTTGGGAAGGGTATAAGGTGACCACAGCACT AGCAGACTGTTCTGGACGTAGTAAGGAGTTC CTGCAGGGGAGGAGTGGGTGAGCCTTTGAA TCCCATATGGTGGTTCACAAGTCAGCCTACA TG	820	D	--
IM000487	CATGTGTTTTTAGCAACTGTGCTCATTTTCTG CTGCTGCTAGGAATAAAATCAAATCTAGTANA ATTGCTTTAATACAAAGTTATTGTCATCCATCT CTGAAGATCTGAAGTATTGCTGGGGGGTCTC CAACTCACCCACC	821	D	--
IM000488	CAAGGGCCTCTCCTCCCACTGATGGTCGACC AGGCCATCCTCTGCTACATATGCAGCTAGAG ACACAGCTCTGGGGGGGGGGTACTGGTTAG TTCATATTGTTGCCCTCCTATAGGGTTGCAG ACCACTTTAGGTCCCTGGGTACTTTCTCTAGC TCCTTCATTAGGGGCCCTGTGTTCCATCCAAT AGATGACTGTGAGCTTCTTATAAGCATAAACT TTCACCTACCACATG	822	R	--
IM000489	CATGGTGTTAGCCTCCAGGCAGGAAGCATAC CAGAGGAGAACTCCACAGGAAGCCTTTGTT TTCTGCTGTTAAAAACAAAGTATGATGGGGCT TAGAAGAGGCTTTAAGAGGTCTCTGGAGAA AAGAATCTATTTTCCATT	823	D	--
IM000490	CATGAGAGGTTTTTAAGTCCTGAAAGACCATC ATACCTAGAGTCTATACAACAAATAAACTTGG AATACAGTGAAGCTAGTAAAAATAACTTCCTG AGCTTATGG	824	D	--
IM000491	CACAGTCAGGAAGCAGAAAGATGAACGTTGA CTCTCAGCTCTCCTTCTCCCTTTAGTTCTATG GAGGTCTCCAGCCCATG	825	K	<i>Fgf3/Fg f4</i>
IM000492	CATGATAAAAGTCTTGGAAGATCAAGAATTC AAGGCCCATAAATAAACATAGTACAAGCAATA TACAGCAAACACAGTAGCCAACATCAAATAA ATAGAGAGAACTTGAAACAATCCCACTAAAA TCAGGGACTAGACAAAGTTGCCCACTCTCTC TTTAACTGTTCAATAGAGTACTCAAAATCCTA GC	826	R	--
IM000493	CATGGTAGCTTTCTAGTGAGGTCTCT TCC	827	D	--
IM000494	AGTACCCTTAGCCAATAAACCATCCCTCTAGT CCCTGTTTGTTTTGTTTTTTTTTAAAGACAGG GTCTCACCATG	828	K	<i>Fgf3/Fg f4</i>

IM000495	CATGAGCTAGGCCATCTGCAAGCTGGTCTCG TCTTGACCAGGAGTACACAGAAGCCTGGCTC AGGACTTGGTAAAC	829	D	--
IM000496	GTTGTTTATGCAGATCTCTCAGCGTTAGCATT CTATGGGATTCTTTGAAAAGACCTTTTCAGTT ATCTTCCATTTCTGAGGCTGTTTCTAGGCAAC GGAGTGGTACCTTCCTTTAATCTTCCCCTGAC CTTTTCTGCCTATGAAGATGTTGACTAGTGAG CCCGTGGGGATGTGTATTATCTGTTACATTTA TTTATGGCTTGGTAGCGACTCCTTGGTTGTTG TTCAGCTTTTCATG	830	D	--
IM000497	CATGCCTCCCTCAGCCTCCTCCCAC CCCTTCCTGTCCTGCCTCCTCATCAC TGTGTAAATAATTTGCACCGAAATGT GGCCGCAGAGCCACGCGTTCGGTTA TGTAATAAACTATTTATTGTGCTG GGTTC	831	K	<i>Wnt1</i>
IM000498	TCTAAGTCCAGTCTTTCACACACACTGACTTT GGTCATCTGTAATCACAACATG	832	D	--
IM000499	CATGCACACAACTGGCCCTGAACTTTTGAC TTCCAGGCCTCTGCCTCTCTGCGCGCACACA CACACTCGCACTCCTGTATATGAAGCGTATAT GTGTTTCTCTGGGAACTGTTTTATCAGGTGA AG	833	K	<i>Fgf3/Fg f4</i>
IM000500	GGGCTGAAGGAAAATGTTGTGTCAT CTTTTGTGGCATG	834	D	--
IM000501	CATGTACCACTTTTGCTAATCCCCTA ACCGCCCCTTGGTAAGCATCTAAAG TGATATATCTCTTGGTCTACTGAAGT TCTGCCCTGTCTCCATCGGGGATTCT TCGGGAGGCTAAAATTATAGACTATT TGTGAAAG	835	D	--
IM000502	CATGTCCTTATGATATGGAAAAA	836	D	--
IM000503	CATGTGCCAAGAGCCATTACAGGCT CAGACTAACATCTGCCTGTAAACAAC GGTTGCTAAGTTTCCAGGGAAGCGT AAG	837	D	--
IM000504	CCAGATGACCTTGAAGCTCAGAGATCTCCTTG CCTTAGCCTCCTGGGATTCATAGCCGCTATG CCTCAAGATCTCCATG	838	R	--
IM000505	CATGTAGTTTGCAAACAAGACATCCCTGGTAT ATCCAGAACCTGAGCTATGC	839	D	--
IM000506	GGATATAGTGTCAAACAGTCTGATGTATTCAT AGGTTTGTATCCATAGTTATCAAATCTCTCAT G	840	D	--



IM000507	CATGTACCACACACAGACTTGGTAATAAGTTA GATGATAATTACAAAAGCAACAAATAAAACCA ACAAAACAAAACAAAGCTTGGTAATA	841	D	--
IM000508	GTTAGGAGCACGAACTGCTCTTTCAGAGGAC CTGGGTTTAATTCCCAACACTCACATG	842	R	--
IM000509	CATGGTCAATGATAAACATTCCAAAACACCAA AACCATCCTCTCTGTACAGGCTATGATGATTC AACTGCTGCCCTTCCTCATTTCTTGTTCCTAA CTCCTACTGAATATTTCTGTCAT	843	D	--
IM000510	CATGATAGAAGACCACGTCTGGGATGGGGTA AGGGTTTCTCAGAGTACCTTGCCCTGGGGCC ACATCCTAAATCTACAACAAAGCTGACCCTA	844	D	--
IM000511	CAAGTTTTTGTAAGGGAGCTAAGAAAGGCAT TGTTGGTTAGGTTGGAAAGAGGGGGCAGGA CCTGGCTCTCGCTTCAGCCCACTCCCCTCTG CCCCCAGCCTCAAACACTTTTACCCTAGCA TAGCAGAAACATG	845	D	--
IM000512	CATGAAGTCACTGGGCAGATGAAGAGTTTTT GTGTGAAGTGGGGCTTTGCCCTTATCATCCT GTGTGTTCTCCTGGTGACCCTCAAGCTTGGC TGCAATGATCCCCACTTACAGAT	846	K	<i>Fgf3/Fg f4</i>
IM000513	GTTTATTACTCCAATGATTCGCACAGCCGGG TTGCAAGTCTAAGGCAGGCTGTCTGCCTTCC TGGAGGTACTTACCCACCTCCCCCTCTGGG GGAGCTCCACTTGGCCATG	847	R	--
IM000514	CATGATTTTCAGTTTTCTTGCCATATTCACG TTCTACAGTAGACATTTCTAAATTTTCCAATT TTTCAGTTTTCTCGCCATATTTACGTCCTA AAGTGTGAATTTCTCATTTTCCGTGATTTTCA GTTTTCTCGCCATATTCAGGTC	848	R	--
IM000515	GTAACCACTCATTTACCTGCCCAATGATGTC TGGGCAAGGCACTTTTAAATTCATATCTACT GTGACTATAGGTGCCCATG	849	D	--
IM000516	CATGACACTGCTCACTGTTGCTCTCTAACCTT GGTCCAG	850	D	--
IM000517	GNGCTTGGCAGAGTAGAGAACTCTTTGGGA AACTTGGTTCAGATCCAGACATG	851	C	--
IM000518	CACCTCTGCCTCAGTTTTCCCTGATTA TCAACAAGTGCTCATG	852	D	--
IM000519	CATGTAAGTCAAGAAAGTCTAGTAGGCGTAG TGGTAAATGCCTTTGATCCCAGCACTTGGGA GGTAGAGGCAGGTGGGATCTCTACAAATTCA AGACTGGTCTGGTCTATATAGTGAGTTCCAG GCCAACCTTCACATTGAAATTCATCTCAAAAC AATAAAAATAGAGGAAGATATAGTCAGGCAC	853	R	--

IM000520	GAAGACATTCATTTTTTTCTTGGGAGGGGATA GAATCCAAGGCTCCAAAGCAGAGTTCATG	854	D	--
IM000521	GACCACGCTGGCCTCGAACTCAGAAATCTGC CTGCCTCTGCCTCCCAAGTGCTGGGATTAAA GGCTGTGCCACCACTGTGCTTACTGATCTCT TTGATGTCCCAGTTATAGCTCTTGGGTCCCC ACCCATTTGTAGGGGGACCCAGGACACCTCA GAGCTCTCCCAAGTCTAAAAAGGCGAGGGTT CCTGGCTCCCTTAATGCCTTATCAAGCACAA CAGAACTCAGGGGCAGAAAATGTTCCCAGGA AGAAGTTAGCTGTGGGGAGAGTCATG	855	R	--
IM000522	CATTTTTCTTTATAGCTGAGTGTTATTCCACT GCAAAAATTTGAATATTCCACTATTCTGTTGA TGAATGTCTAGGCTGGTCACGTTCTCTTGCC TTTGTGAATGGAGCAGCAATAAACATAAGTG GGCATG	856	D	--
IM000523	CTCCATTGGGCCGAGTGAAGCTGTGGTTCAG AGAACTCTATGGACAAGCTTGACTTCCAGA ACATTGACCTGGTCTCTGAGATCAACAAGCG TAGGAAAGCCATG	857	D	--
IM000524	CATGGGAAAGTAATCCGTGGCTAACACAAAG GGGAAATAAGTAATATT	858	D	--
IM000525	CATGTAGGACCCTGAATGCCAGCAATGAACA ATACCAGCTTGGTTTTCCGACTCTTGCTTTCT CCTCCCTCCACTACTAACTAGCCTCACCGTT GCATCTTGTGACTCAGAGGTCTTGTTCCAG GGCTTCCTTCCTTCCAGTGTTCTTCTAATGCA TCTAAAGTGAAGGGGTGG	859	D	--
IM000526	CATGCAAAGCCTCTGCAGGGCCGACAGCAA GGAAGGCCCTTCTAGATCTCCGACTCTGT CAAAAGCCATCACTCGGCAGGCAGGCAACCA CAATGTAGGGAAGACCTGTAAAGCCTTCAGA GAGGAACAGCTGGCAGCCCCGGGTCACTC AGAGTGGCCAACAGCTACTCTTGTGGAGACA GCAGGAGGAGGCCTAGACTATAGAAGGATG GAGGAC	860	D	--
IM000527	CATGCACACAAACTGGCCCTGAACTTTTGAC TTCCAGGCCTCTGCCTCTCTGCGCTCACACA CACACTCGCACTCCTGTATATGAAGCGTATAT GTGTTCTCTGGG	861	K	<i>Fgf3/Fg f4</i>
IM000528	CATGAAACATTATTTNTTTTGGAAAGT CTGCAGGTAAACTTAAATAGGTTAA	862	R	--
IM000529	AGCAAGAACAAAGGAAGTACTTCACCTGATA AAAACAGTTCCAGAGAAACACATATACGCTT CATATACAGGAGTGCGAGTGTGTGTGTGAGC GCAGAGAGGCAGAGGCCTGGAAGTCAAAAG TTCAGGGCCAGTTTGTGTGCATG	863	K	<i>Fgf3/Fg f4</i>

IM000530	GATTTTATTTTCCTTAGCATCCTGATTGGAG ATGCCTGGGTGCACATG	864	K	<i>Fgf3/Fg f4</i>
IM000531	CATGTAGAGACTGCCATATCCAGGGATCCAC CCCATAATCAGCATCCAAACACTGACACCATT GCATACACTAGCAAGATTTTATTGAAAGGACG CAGATGTAG	865	R	--
IM000532	GACCTGTACCCTACCCTCTGATGGAGGCCAT CTATTTGCCTGTCCCCAGGAGTCCCCAACT GCTCAAAGAACAGACTGTGGGCTCTGGAAAG CTAGCAGGTGACCCCGGGGATGTTCTGAG CAGTGCCTTACTGAAGTTTATCCAGGCCCTA GGTCCCCTCAACTGCTCACACAGCCTAGGG TGGGTCTCTTGAGGAGTCACTTGCACTTCT GTTGCTTCCCAAGAGACCCAGGGAAAAAAGG AAGGAAGGCCATG	866	D	--
IM000533	ATCTCACTCGTAAAAATGAACAAAGGGACTGC AGAGATGGCTCTGAGCTTTTAAGACCATAGC CTGCTTTTCCAGAGAGCCCAGGCTTCATTTT CCAGCCCACATATGGCAGTTCACAACCATCT ACAACTCTAGTTCCTGGGGATCTCACACTTTT GTCTTCTGTGGGCACTGCGCAAATGTGCACA GAAATACACGCAAGGAAAACACCCATG	867	K	<i>Fgf3/Fg f4</i>
IM000534	AAGAAACACTCTTAGCTGGGCCTGGAAGTGC ACATG	868	D	--
IM000535	CTAAAGCAGATTATTATACTTATTCTACTGAC CATAATGCAACCACTATTATATAAACAGAACA TACTATAAAGTGAATAACATTAGGATACAAA TGATATAAAGGGGAGAGAGGATAACCATTGT GAAGTATGTTTAAATAAAATGTTTGGGATTTG AGGAAATTAATAAATTAGTTACCCTTTTTGCTT TGGGGAAAGAAAGGCAGCATG	869	D	--
IM000536	CAGCCCCAAACCCATCAGCCTGAGACTGATG CACAGGAGGCAGGCCAGTTAGTTATTCTCTG GGCCCTCTATTTTGCCTTCTGTAGGTTAATC CCACCGCTCCAGTGCTGGAAAGTGCAAGCA TTGTGGGAAGTTAAAAACGTGCCACCATG	870	D	--
IM000537	CATGGACAATGCACCCCTCAAGCAGTGTCTT CCATACAGACAAGCATATTTATTTTCTATACA GACAGCAACTTTGCTGAGGTGTAAGG	871	K	<i>Fgf3/Fg f4</i>
IM000538	GGATGAAGAAGCCCAAGGTATTAGGTCAGTC TTGCTCTGACTTCTCACAGTAAAAATACAAC CCCAGGGACTAAAATGACACAGAACAGCTTA GCCTCTGGACATTGCTTTTGGATTGCAAAGT GATAAGTGAAAAAGTAATAAGTCTATCTACAT TGGAACACATTTGGTAACCTTCATTTAAACACA CTTCCCCATG	872	D	--
IM000539	CATGTCCTACATTGGACATTTCTAAA	873	R	--

	TTTTCCATCTTTTTCAGTTTTCTCAC CATATTTACGTCCTAAAGTGTGTAT TTCTCACGTGTATTCGTTGGTTGTTG GTTTAGTTCCTGGGAGCTCTGGAAAT CTGATTATT			
IM000540	TGGAAATGAGAAACATCCACTTGACGACTT GAAAAATGACGAAATCACTAAAAACGTGAAA AATGAGAAATGCACACTGAGGGACCTGGAAT ATGGCGAGAAAACTGAAATCACGGAAATG AGAAATACACACTTTAGGACGTGAATATGTC GAGGAAAACTGAAAAGGTGGAGAATTTAGA AATGTCCACTGTAGGACGTGGAATATGGCAA GAAACTGAAATCATG	874	R	--
IM000541	TGACATACAGAAAGAACACAAATACCTGTAG CTGCTGTGACAGGACCAACCATTCTAAATATC AAAGCAGCTGTTGACACCTAAGGACTGGTCT GACTGCTAGATCTAGGAGTTTCAACTTGCAAA AGCTGGCTTGATGCTCATG	875	C	--
IM000542	TTATATATATATATCGTTTTCTCTTACTCCTGA ATCAGTGACATG	876	D	--
IM000543	CATGTCAGCCCTCAGCTTTACACAGGTGTCA AAAAAAAAAAAAAACTGACTGAGATCTTCC GTCTGCCATTAGCTGTTATTGTGTACATTAAG TAGAATCCACTGCTTAACCCAGGCTACTGGG CTCACCCAGTATTCAAGGAGGTGCCACAGG ACTCAAAGGATACAGAAGTTACATATTAAC CCAATCTCGTAGAGGATTCAGAGGAACCTAAG TTTGGTAGGGGCACAGATTGTAGTACCATTA AGCCCCTCTGTTCTCGTGGAGAACCCTAC TGTCCAGCAAGGCGGGAAGGACCCAAATCAA GCAATGAGACTTGTTCTGG	877	D	--
IM000544	CATGATANATCCCTTTTTGTGAGCAT TCCATAGCCTCAGTAATAGTGTCTGA CCTTGGGACCACGCTGTATCCCACT NTGGGACCTTCTTTTCNTCAGGCTAC TCTCCATTTCCATTNCTGTAATTCTTT CAACAGAAACATTTATGGGTCANAG GTGTGACTGTGGGAGGACAACCCCA TCCCTCACTTGATGTCCTGTCTTCCT GCTGGAGGTGGGCTTTATAAGTTCC CTNCCCCTACTGNCCAGCATTTTCATC AAAGATCCCTCCCTAGGAATCCTGG GAACCTCTC	878	D	--
IM000545	GATAAGCTTATCTTGAACCTTGAATGTATATGG AGAAGCAGAAACCTTGAAACAGCCACAGAA ACTGAAGAAGGATGAAGGTGGAACCTCTCAGC TGGAATATTCATG	879	D	--
IM000546	CATGTTCCCAGCTGGGCAAGGCCTCGGGTTC CTCGGTGAAGAGTGTGGACCAGCCGATGAG	880	B	AI4132 88

	CCCTCCGACGTGTGGATGAAACGGCTGGCTT TTGTTTAGTTTTGTTTTAACCTCCCCAACGAG ACTTTGATCAGCTCCACCTCGAAAATGTTCCG GAAAGATGCGGAGAGCCTGAGGGACTGCGG GGCAGCAACGGGCTCCGGCCTAGCCCGGCC CGCCGGCCCCCAGA			
IM000547	ACCAAGTGTTAATAATGTAAGTGGCTTCTG CCTGTGGCAGTACACTTGTCTCTACACATG	881	C	--
IM000548	CCTTACTGCAGAGATGACTCGGCCAACGGCT TCGAGCCCCTGACCACTTCTCAGGTTTGGT TTTGTTAGTTTTTCTCACAGCAATGGAAGC ATAATCAATACAATTCCCAGAATGCGACCTG TGACAAGGCCAATGAGCAGACTCAAGGCTGG GCACATAAAAGCACCAAAAAAAAAAACTCCCT TGCAGTTATTGTTTCATG	882	D	--
IM000549	GACTGAGCCTGCCTGGGGCCGCTAG GGAAGGGGGGGTTGGACCCTCTGG TATTTGCAGTTACCACTGACAGGGTT TTTCCGAGATGCCAGTGTGAGGGTG TTCGGTGCTGACCCCCAGGGACCG TGCAGCCCCGATGGCTGTCTCGGTC CTCTCANTTTTTCCGCCACCCCTGG GATATTTGAGGACTCANTCCCCGCAA CAGCTCTGACTGAGGTCAGCTCTGT GACCAGGGNCCCTGTCCCCGGTGT GNNGTGTATTTGCATG	883	K	<i>Wnt1</i>
IM000550	CATGTAGAAGGCAGAGGACAACCTTCAGGGA TTATTTCTGCCCTTTTAC	884	C	--
IM000551	GTTCTCCATTCTGCTGCTTCTCCCTGATACA TTGAGTTACAGCAGCCCACGCGTACACACTC TCGCACATG	885	K	<i>Wnt1</i>
IM000552	CATGCCACCAACAAATAAGTAAGTAAAAAGA AGGAAGGAAGGAAGGAAGGAAAGAAAGAAA ACATTTTAAATCTGTAAT	886	D	--
IM000553	CGGAGCTTAGGTCTATCATTTAAAGATACAAC CAAATAGGCAGAAATCATTTCTGAGGAGCCC ATTTTCTTTATCTCAGGTCCTGCAGATTTCTC CCTGGTATTATCAGGGAGGAGCAGCAGCTGA GCTATCCTATCTCCTTTACTAATAGAAAAAAC GCCTTTAGGGCTTGAGCACAGGACCTGTATT TCAGGGGAATGTTGACAATCCATAACTCCAG GGTGGACTACTAAGCCCTGCAAGGTGAGTGA ACCCCGGCCGAGAATAAGGCCCATG	887	R	--
IM000554	CATGGCCTGAGAGTTGAAAAGATATTGTAA GCAGGGGTTGTTCCAGAAAGTTTAGAATATA CAGACACTATACTCTATCCAGACTTCTTGGCA CAGGGAGTTCAAATGTAGACTCTGAGCCCCG TCCTGGGGCAGCTTCTTCCACCTGCTTTGGG	888	D	--

	TAGAAGCAGGCAGACTCTGGGTAGACTCTGA TTCCAAGGCTAAGTAACCCCTGAACCCAGAA CAGTGTTTTT			
IM000555	CCAGATATCATACTGAGTTCGTAGGTGGTTTT AATTAATCACGGGCCCTGGCATG	889	D	--
IM000556	TTGGTGATCCAAACCCAAAGAGACAAATGCT GAATGTTCACTCTCATTTTCTGTTCTTAGCTC CAAATCTTCAGATATGAGTAAGCAACACATAA ATTATGAAGGGACCATACTGGGATGTAGGGG GCTTGCATG	890	D	--
IM000557	CATGAGCACTGCTCTAGGGACACCT CCCATCCCTTCCTAGCACCCCAAAT GCCCCTTCCCATCTCTCCTTCCAGAA GTTGGA	891	K	Wnt-3
IM000558	ATATAGCTGTCTCCTGAGGGCCTATGCCAGT GCCTGGCAAATACAGAAGTGATGCTCACAA TCATCCATTGGACAGAGCACAGAGTCCCCAA TGAAGGAGCTAGAGAAAGTACCCAAGGAGCT GAAGGGGTCTGAAGCCCCATAGGAGGAACA TCAATATGAACTAACCAGTGCCCCCAGAGTT CCTTAGAACTAAACCACCAATCAAAGAAAACA CATG	892	R	--
IM000559	CATGATAAGGTTAGAGTTTTGTGAGCCTCCTT AACCTTGCTCAGCAAGCGTTGGGCTCTTGGC AGCCGAGCTGCCATCTTCTCATCCCCGATA GAGCCAGCCGCCCTTGTCGTGTCTTGAATAA GTTAGAGGAGGCATTATAGAGCGGACCTAAA CATTTGCCTTGGAGCCTGAGGGATGGGGATT GGCTGAATGTGAAT	893	D	--
IM000560	CAGAACTGTGCTCTTTAGGAAGCCAGACGCT ATGCCTTAGGCCCTGTTCCCTCCAGACCTTG CTCTGTGCTACAGTGTAAGCGAAGATCAT G	894	D	--
IM000561	GAGAATTAGAAAAGAGATAACAAAGGCGAGA AAGAGAGGCGTGTGAGAGCATG	895	D	--
IM000562	GTTTCCAGATTGTCCTAGTAGCTGGGCTGCA GGAACAGCCAGCATG	896	C	--
IM000563	GGGGGTGGGGGTGGTAAGAGAAGATTAATTA GCCTAGCATATATAAGGTTTTGGATTCAATCT TCAACTCCACCCCTTAAAGAATAAATAACAA GTAGATAGATTATAGACAGACAGCTAGATGG ATAGACAGATAGCTACATAGATACATAGATAG ATGATAGATAATAGACAGACAGACAGATAAAT GATAGATAGATGATAGGAAGTCCCAGTTAAC AAATGGAAAATAAAAAGACAAAAGTCCCCTTG TCCATG	897	D	--
IM000564	GTATATGGAATATGGCAAGAAAAGTGAATATC	898	R	--

	ATG			
IM000565	CATGGTAAAGGTCAGGAGTACACCTGTGCTT CTGTGTTCTTCTGTGTTGGCTGACAGCTGGG CAGAAGTGAGTTCAGGAGGNCAACCCATACG ATGAGACAAGCCGGGGCAAAGTGGGATATGT GGACCGCAGCACATCAGAAGGGTGTGCCCG ACATAAAC	899	B	AA1113 54
IM000566	CATGAAGTATATTATTAGAGGGGAAGTAGTCT TACTGCTGAGCAGCGTGTGTTCTTCTACAGA GGATGTTTGTGTTCTGGAATTTAAATTAAGT AAAGTAATAGTGTCAATGAAACGTTGTCCGGT GACTTGCTTCTTTAAATGATCACTGTTAGAC AGGGA	900	R	--
IM000567	AATAATCAGATTTCCAGAGCTCCAG GAACTAAACCAACAACCAACGAATAC ACATG	901	R	--
IM000568	CATGATTTGATAGGGTTATTTGGTCTCTGGA ATCTAACTTCTTGAGTCTTTGTGTATATTGG ATATTAGCCCTCT	902	R	--
IM000569	GCAAATAGTCCTTTGTACCGAAGTCCACACA CTAATGTAGTGAATTATTTAAATTTATTCCTT AATCTTTTTTAAAGTCCAGACTCTATCCCC TCCTTGTCACCCCTCTGATTGTTCCACATCCC ATACCTCCTTGCCCTCATG	903	R	--
IM000570	TTCCATCTCTTGATTCTGTTGCTGATGCTCA CATCTATGTTTCCAGATTTCTTTCCTAGTGTTT CTATCTCCACTGTTGCCTCACTTTGGGTTTTT TTATTGTGTCCACTTTCCTTTTTAGGTCTTG GATGGTTTTATTGAATTCATCACCTGTTTGG TTGTGTTTTCCTGCAATCTTTAAGGGATTTT GTGTTTCCTCTTTAATGTCTTCTACCTGTTG GTTATGTTTTCCTGTAATCTTTAAGGGATTTT TGTGTTTCCTCTTTAATGTCTTCTACTTGTTA GCAGTGTTCTCCTGCATTTCTTTAAGTGAGTT ATTTAAGTCCTTCTTGATGTCCTCTACCATCA TCATG	904	C	--
IM000571	CATGAGTTTTCTACTTTTTATAAAATTATATA AAGTCATTTAGTAGAACCTAGCTTTATTTAATT TTACCAATTAATATAAGGCCACTGATATTATT GACTTTTGTCACTACAAAATACAGCAATGAAA TAATCTTTCTTCTAGGCTCCTTCCTCATCAAA CTAGTTCTTCAGCTCACATTAATACTTTTTCA AGTTGTAAGGGACCTCAGGGACAGGGGGC	905	D	--
IM000572	CATGAGCTTATAGTTTCAGTAAGAGAGCATAG ATAGAATATAGGTGCCTGTGCGCTGGCTCTT TTGGTTGTATTTAAATCCTTTATCTCTGAGAA GTCGGAAGTGTGGCAACAGACAATATGGTA GCC	906	D	--

IM000573	CTGACACAGGTATGCCAGTCCATAGTGTGC AGAGCACAGATGGCCAAGGATAACTAGGAAT GAGACCTACTTAACCCAAACTCCAAACATTAT GAAACTTTAAAAAATGACTTCAGTTGAACTT TGCAGGTAACCATCATG	907	D	--
IM000574	ATTGTGTCCTTTTAACATTCTTGCTTTAGTAGA ACATCCTCTGACCCGTATCTGATTCAGTGAAA AATTCCTTCACGAGTCTGCCTTAGCAAAACAT CCTTTCACCTGTGTCTGCTTCAGGAAAACAC CCCTTCACATG	908	R	--
IM000575	CATGTTGGTAACAGATACAACAAGCAGACTTA AACTAATAAGAAAACAGCTATGATTAATATGT TTATACTTAGCTGAAGAGAATGTATGGAGCT TTGAAGTTAATCTTTTCATATACACAGGAATG CCTTCAAAAAGCATTGCAGCAGATTTCAAAG GATTAACTCAT	909	D	--
IM000576	CATGTGGCGAACCAGCATCACTTTTGCTCTTT CCTTACTAACCAGGACATCCATCATTATTTT AATAGCATCCACCCTAGTAGATATAAGGTGAT ACCTTATTGTGATTTCACTTGCTTTCTCTGAA GATCACTAACAATCAAAATCTGGTTCATTTTA TTTATGAATTCTCATTGTCTTTTGCTAAATAT ATGTTCACAATTCTTTTCAATTTAAAGCAAAT TGTTTTGTTAATAATGAGCTAACTTTTCATACA TTGAAG	910	D	--
IM000577	TTGCTGTGGGCCTAATTCAAGGCTG ATAGATCACCACAGAAGGACACTGTT TTCCTCCGGGCAGCAGGAAGTACAG GGTAGGGACTCTAGAATCACTGCCC TAGGGCATG	911	B	AI6639 69
IM000578	GTAAGTGAAGTTTATAGCTAGAGCAAAAAGACA ATGGAAGGAGATCAAGGGAATACAAAGTGGG AAAGAAGTCAGAGTATCATTATGTCCAGGTG ATATGATAGTATACATAAATGACCCATAGAT TACACCTAAGACCTCTACAGTGGATAAATACT AAAATATTTACTACACAGAAATCACCCCATG	912	R	--
IM000579	CATGCAAGGTATGAACTCACTAATAA GGGGATA	913	D	--
IM000580	CATGGTTCACACTCCATAATATCTTGTTCTCA CTAATTCCTCTAATCCCATAATATACACCAAT AATTTAACAAGGGAATTTCTACATTGATTTGT AATAAGGGAGATACTGTGTGAACTTACCCAA CAAAAGTCTCCAATAGAAGTGTGGATACAC AGGAAGTCTTGACACACCAATTAATTTGGG TCTGATAAGAAGATAACCCCTTAAATATATAG ATTTATGTAAAG	914	D	--
IM000581	CATGGGCTGGGGAAAGGCAGAGAGAAGAAC ATCTGGATTGTTCTTAACCTTTGCCTTTAAAT	915	D	--



	GAGACTTCAATAACTTAGACGTACCAGCTT CTCACAGTCAGTTAAATGTGACACACACAC CTCTCAGCAGACTGAATGGGTGAG			
IM000582	AGAGATGGTTGGGATTTAAGTTACCA GGGTAGGGTCACCACAATCAACCCT TGATGCCTTTATAGGAAGAAACATG	916	D	--
IM000583	CATGGAAGTCTAAAAGACATTAGGTTCTGGAT GGAAGAAGAGAAAATTATCTTTAAGTTTTAGA AAAGGGATGATAAAACAAGTCTTAAATCTTCT CAATTTTGCCATAATTCATTTGAATTAATATTG GTAAATGCTTTGTGTGGTCCCATAAAGTTCAA TGTGTTATATCACTAAGTAGTTATTTGTAAAAT TATAAATAGCCTCTAT	917	C	--
IM000584	CTTGTGAATTGTTTAACTGTTTTGAAAAAGTA GATGTTTTCTCTATTTATTTTTGGGACAATTAT CAGAATTTGAAACAACTGTGTATCTCTTATT TACTTTCTGCTTAACCCCCATG	918	D	--
IM000585	CATGGTTGCTATATTCATTAACACAAATCATT AAAATCCTTAATGTAAAATGGGCACATTTTCA AAATTAATAATATGAAAACCAATAAGATAG AAAATTTAGGAAAAAAAAATAATCCAAGCAAGA TGTTAACATCCAACCACAGCAGCATATTAGCA GCAGGACAAAAATAAGGACAACAACCAAGAA AGGGATTGTGGTTAATGTATGCCTCATTGGA AGGGATAATAGGATGTAAAAGTGTGACAATA AAGAGAAAAAATCTCTTTTAAATGTAAGTT AAAATAATAAAAAATAATTTAAAAATTGGTGTT TCAGGGCTGGATAATATTACTAACAAAACCAG GGAATTATTAATAAAAAATCTCTTATCAGTTAT	919	D	--
IM000586	AACAAGTTTTAAATGGGGCATAGTGGATCAC ATTTGTGATCCCAGCACTTGGAAAGGTAGAAA TAGGTAAATTAAGAGTTCAAGGTCATTTCTCA GTTATGTAGTTGTACATTTCTAGCGATGTAGT TGAGTTCAAGGCCATG	920	D	--
IM000587	GTCCTCCAATGTGCATTTCTCATTTTCACGT TTTTCAGGGTTTCTCGCCATATCCATG	921	R	--
IM000588	AATTGCATTGAATCTGTGGATTTCTATTAACA AGATGGCCATTTTTTCTATGTTAATCGTAC TGATCCATCAGGATGGCAGTCTTTCCATCTTC TGATATCGGCCTCAATTTCTTCTTCAGGGGC TTGAAGTTATCGCCATG	922	R	--
IM000589	GGCTAGGTACTCCTAAACCTTCTCTGCTATC CTAGGCCCAATAGAAAAAAGTGGCCCATG	923	D	--
IM000590	AATAATACTTTCACTGTACTTTAAATATTATC TCCTATCTCACTCTAATACTTCTGTGAAAGAA GCAATATCGTCTCTTTGTAGATAAAAAATGGCT GAGAAGGGCACCTTCAAGACACTAAGTGACT	924	D	--

	AACTCAGACTCAGAAGTTCAGAGACCATG			
IM000591	CATGCTCTACTATGTTACAGCAGTCTTATTT ATAACTTCCAGATACTGGAAGCAACTCAGAT GTTCTCAATGTAAGAATGGATACAGAAAAA TATGGTACATTTACACAATGGGGTACAACCTCA GCTATTAAGAACAATGAC	925	R	--
IM000592	AAAACCCAAGAACAATTAAGCTGTAG TTCCCAAGTGTAATTATATTATGGTT GTTTCTGCTTGCTTTATATCCCTATAT ACAATTTATGATTCAAGTATTAGTGG GAATAGACTAATGGCATG	926	C	--
IM000593	CATGCCAAGCCTTCTGGTATCACCCCTAAAGG C	927	C	--
IM000594	CATGCTCTTCTCTGCTGTTCTTACTGAATTTT AATAAGAACAATTCCACACAGCTCGAAAGCA CTGCTCAATTAAGAGATATTCCTACCAGGCAT CTTTGGAATCCTGCAAGCACCTCTTCTCTGTT TCCTGATGACCCTCAATTTGGTTGTGTCCAGA GGTTGGTGGGGAGGAGGGGAGGGGAAACG AAGCTATTTTTTTTTAATTGCAAGTTCAATT TACAATGTTCTCGAT	928	D	--
IM000595	CATGCTAGGCAAATGCTCCACTGAATGAATTA CATTTCCAATCCTTTAGATGCATTTTAAAGAG AAAAGATTGAGTACTGAAGTTTTGAATAGAAT ACAGGAATAAGGGACTAAACATATATATAGCC TTATATAGAGAAATATTAAGTAAGTAGTAACTT TGCTTGTGTGTGTGTGTGTGTGTCACAC	929	D	--
IM000596	CATGCCATTAGTCTATTTCCCACTAATACTTGA ATCATAAATTGTATATAGGGATATAAAGCAAG CAGAAACAACCATAATATAATTACACTTGGGA ACTACAGCTTAATTGTTCTTGGGTTTT	930	C	--
IM000597	CATGCACAGCTGGTGAGTGAGTTGTCTTCTG GTACAAAAATCTCCTCACAGGCACATTTACAA GTGCCTATATCTTTGCTAGCTTCAAGAACACA AAGAAGGGACACACAAAAGCTCTTCTGAGTC TCCTTCTCCTGCTGTTATTTTG	931	D	--
IM000598	ATCGTCAAAGTTAGCAAAATTATAAATGTGAA AGTCATG	932	D	--
IM000599	CATGAATTATGTTTGTTTTATTTCTTT TGTACATCATTCAATGCAGTAATCTA AAGTTTGGGGTCTTGGTCTTATATCT TGGAACCTTCAGTGACTTATTGTTCT AACG	933	D	--
IM000600	AGAGACAGTCACAAAAGGGGCCCATCTTGT TAAGAATGGGCCAGTGAGAAAGTTCGGGTTA GTGGAGTAGCCTGCCTCAGTTTCCTCCTGTC TTCTGTAGTTAAATGTGTTAATGGTTAACATG	934	K	<i>Fgf3/Fg f4</i>

IM000601	CATGTAGCATTTATCTTAGCCAGCAC	935	D	--
IM000602	CATGTACAGACTATGAACAGGAAATGTTTTG CAAATAACTCTGTGCATTAGAATTTCTTCAG AAATATAACCATTTTGACAGTTGTAGGTTACA CTTTTAAAATTACAAAATCAATAAAATTGATCT ACAAACCGAGGCCTACAAAACCCTTGCTGGA TATTGAAGACGGCATAATATTAAG	456 936	D	--
IM000603	AATTCCCACCACCCACAGGGTGGCTCCATAA CCATCTGTAACCTCAGTCTCAGGGACTCCAA GGCCCTCTTTTGGCTTGCAAGGGCTTGACACA CACACAGCGCACACATG	937	K	<i>Fgf3/Fg f4</i>
IM000604	CATGGTGAATGATTGTTTTGATGTGTTCTTGG ATTTGGTTTCGAGAATTTTATTGACTATTTTGG CATTAATACTCATAAGGGAAATTGGTCTGAAG TTCTTTCCTTGTTGAGTCTTTATGAGGGTATC AATATAATTGTGGATTCATAGAGCAAGTTAGA TTGTGTTCCCTCTGTTTATATTTTGTGGAATAT TTTGAAGAGTATTGGTATTAGATGTTCCCTTGA AGGTATGATAGAATTCTGAACTAAACCCATAT GGTTCTGGATTTTTTTTGGTTGGAAGACCAAT GACTGCTTCTATTTCTTTAGGTGTTATGGGAC TGTATAGATGGTTTATCTGAACCAGATTTAAC TTTGGTATTTGTTATCTGTTTAGAAAATTGCC CATTTTCATCCATATTTCCCAGTTGTGTTGAGT ATAGGCTTTTGTAGTAGGATATAATGATTTTT GAATTTCTCAGTATGTTTTCTTATATCTCCCT TTCCATTTCTGATTTTGTTAATGTGGATACTAT CTCTGTGTCTCTGTTTAGTCTGGCTAAGGG TTTTCTATCTTGTTGATTTCTG	938	R	--
IM000605	CATGGGTAAACAGTGGGCCCTAAACTTGAAC TAGAAAACCTAAAGATGCTCATAGGGAAGAA GAAAAGAGCAGAAAGCTTAGCTTCTAGACAG GGGTAAGGCTTAGAGCTCAATAAAAAAGGAA CCCC	939	K	<i>Wnt1</i>
IM000606	CATGGCCTGTCTCAGTTTACTTCACAGCTGAA CAAGAGGCAGAGAGTGACAGGTAG	940	K	<i>Wnt1</i>
IM000607	CATGCTCGCCAGTCCCAGAACCTGG AAGGCTGAGGCAGGAGGATTAAAAA GCCTTGGGGACACCAGGCTTGGTGG CACCGGTCGTAAATCCAGCACTGGG GAGTTAAGAAGCAAGTGAGTCACAT CTGTGAGTCTGAGGCTATCTTGGTCT ACGTAACCAGCTCTAGTATAGCCAG CCTGGGATACATAGTAACCAGTTCTA GTATAGCCAGCCTGGGATACACAGT AACCAGTTCTAGTATAGCCAGCCTG GGATACACC	941	D	--
IM000608	CATATGCGTATTACATTTGTGTGGGAACGTC CTTGAGAAAGCAGGAGCAGGAGTTACAGAC	942	R	--

	AGTTATAAGCTGCCTGACCTGGGTGCTGGGA AACACCTCAGGTCCTCTGGAAGAGCAGTAAG TCCCCTTAACCAATGAACCATCTATCCGTCCA GCCTACATTTAATTTGTTTTCTATTACTTTG TCTGCATG			
IM000609	CACACACACACACACACGGCTGGGGATCCAA CCCATCTCGTCCTTACACGTGCTCTACCATCA CGCCACACATTTCCAGCACNTTTATCTGAAGT GTTTCCTTTTATTTGTGCATG	943	K	<i>Wnt1</i>
IM000610	CATGCCTGGTGCCTGCAGAGGTCAGAAAGTG TTGGATGCCCTGGAATTAGAGTAACACATAG TTATAAGATGCTGCGTGGGTGCTGGGATTTG AACCCCTTGTCCTCTGCAAGAGCAGCCAGTGC TCTTAACCACCGAGCCATCCCTCCAGCCCT GATTACTCACTCTTCACGGCCTCAATCTTGTA AGGAATATTGAGGCTGCCAAGTGACGCAAGA GCACCTAGGAAGGCAGCCACATCGGTGGCA CTCTGGAAGCACTGCGAGGATGACTGCACAC ATTGCCGGTTGTC	944	K	<i>Notch1</i>
IM000611	CATGCTGGCCATTTATTTTGATTAAAGTTATA CTCTAGACCTTTGTAAATATTAGCCATTGCAT ATTACAGAAATTTCTTAGCAGAGATAGTCTCT CACTCTTAGTGATGAGCAAGCTGGAGCTCAG CATTATTCTCCAGCTAAGATACAGAATTACA GACGTTTATGACGGACACATCTTGGATGTAG TACTTAGTCCAC	945	D	--
IM000612	CCCCCCCCGCCCTGCCAGACCGCAGCCCC AAGCACAGCATG	946	D	--
IM000613	CATGCCTCCCTCAGCCTCCTCCACCCCTTCC TGTCCTGCCTCCTCATCACTGTGTAATAATT TGACCGAAATGTGGCCGCAGAGCCACGCG TTCGGTTATGTAAATAAACTATTTATTGTGCT GGGTTCCAGCCTGGGTTGCAGAGACCACCC T	947	K	<i>Fgf3/Fgf4</i>
IM000614	CATGAATTCAATGGTGTGCTTGCTATAAATGC AAATAAACCATATATATCATATTACACTCAATT TTAAATATTTTCTTAATATTAATAAAGGTGAT GGGGAACCT	948	D	--
IM000615	CATGTCTACTTTATTGCATATTAGGA TGTCAGGTCCTGCTCGTTTCCTGGG ACCATTTGCCTGGAAGACATTTTCC ATTCTTTTACTCTGAGATAGTTCCCTG TCTTTGTTGTTGAGGTGTGTTTCTTG TATTCAGCAAAATGCTGGATCTTGTT TGCGAATCCAGTCTGTTAGCTTATGT CTTTTACAGGTGAATTGAGTCCATT AATATTGAGAGATATTAAGAGAAAT GACTTTTGGTTCCTGATATATTTGTTT TTCTAGTTAGTTTGTGTGCTTGGGA	949	D	--

	CTCTCTCCCTTTGACTGTGTTGTGAG ATGCTTAATATCTTGTCTATCTTTG GTGCAGGTGTCTTCCTTGTGTTAGA GTTTTCAATCCAGGTTTCTCTGTAGT GTTATGTTAGAAGACATATACTGCTT GAATTTAGTTTTGCCTGGAATATTTT GTTTTCTCCATCTATGTTGATTGAGA GTTTTCTGGGTAAAATAGCCTANCC TGGCATTTGTGTTCTCTTAAAAGTCT GTATGACCTCTGACTANGCTTTTCTG GCC			
IM000616	CATGGTGAATGATTGTTTTGATGTGT TCTTGGATTTGGTTTCGAGAATTTTA TTGACTATTTTGGCATTAACTCATA AGGGAAATTGGTCTGAAGTTCTTCC TTGTTGAGTCTTATGAGGGTATCAA TATAATTGTGGATTCATAGAGCAAGT TGGATTGTGTTCTTCTGTTTATATTT TGTGGAATATTTGAAGAGTATTGGT ATTAGATTTTCTTGAAGGTATGATA GAATTCTGAACATAACCCATATGGTT CTGGATTTTTTTGGTTGGAAGACCA ATGACTGCTTCTATTTCTTtaggtgt TATGGGACTGTATAGATGGTTTATCT GAACCAGATTTAACTTTGGTATTTGT TATCTGTTTAGAAAATTGCCCATTTT ATCCATATTTCCAGTTGTGTTGAGT ATAGGCTTTTGTAGTAGGATATAATG ATTTTTGAATTCCTCAGTATGTTTT CTTATATCTCCCTTTCCATTTCTGATT TTGTTAATGTGGATACTATCTCCGTG TCCCC	950	R	--
IM000617	CCATGTCAGGTGGTTAACCTGTGAGTCTAAC TTCCAGGAATGCAATGCCTCTGGCATCTACA GGCATAAACATACTTGTGGCTTACACTCAAAC TGACACACCAACACATATGTGCACGCGCACA CACACACACACCAAATTAATAATAAACCC CTTTTTAAAAAATATAGAATCTATAGATAATT GCTTTACTGCACTCACAAACATTTTAGGATC	951	D	--
IM000618	ACACTAACACAAAGAAGGGGATC	952	D	--